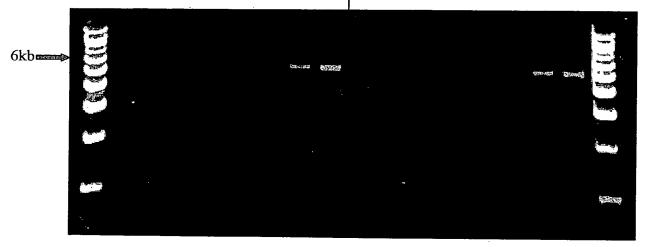
Chimeric blend A

Chimeric blend B

pH 5.0 7.0 7.5 8.0 8.5 9.0 9.5 10.0 5.0 7.0 7.5 8.0 8.5 9.0 9.5 10.0 M



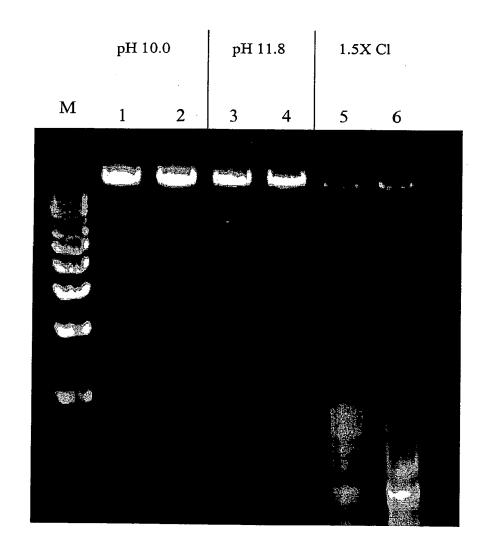
6kb BG 15"/kb - 1'-30"

1X Cloned buffer

pH 9.5 10.0 10.5 10.8 11.0 11.5 11.8 12.0

M

19kb BG 30"/kb - 9.5' extension



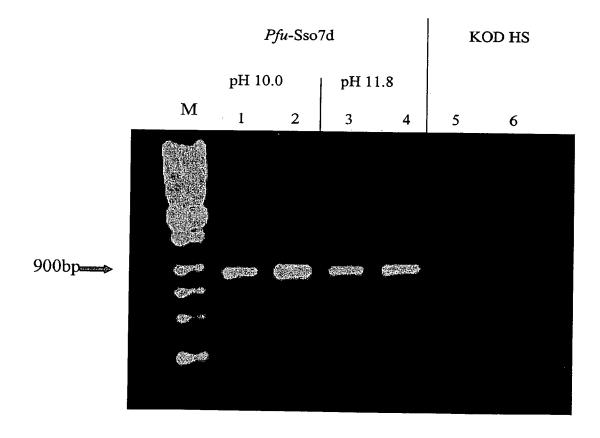
19kb BG 30"/kb - 9.5' extension

		Pfu-Sso´ pH	7d blend [10.0	5	Sso7d 10.0	Hercu	lase		culase DMSO
	М	1	2	3	4	5	6	7	8
19kb	e de la companya de l	A CASE OF THE PARTY OF THE PART	a in the second						

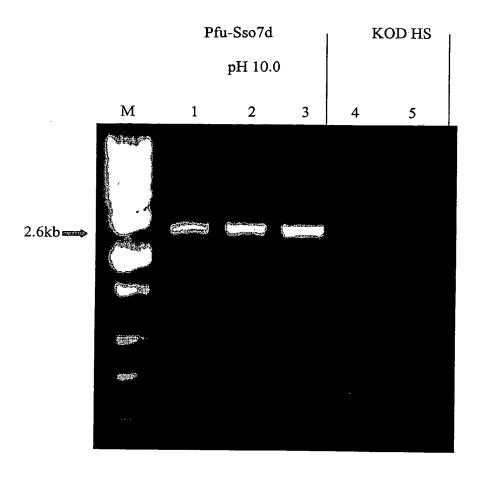
19kb BG 30"/kb - 9.5' extension

		Pfu-Sso7d pH 10.0				Hercu 3% DN	*	KOD HS		
	M	1	2	3	4	5	6	7	8	
19kb 		,			March Stude					

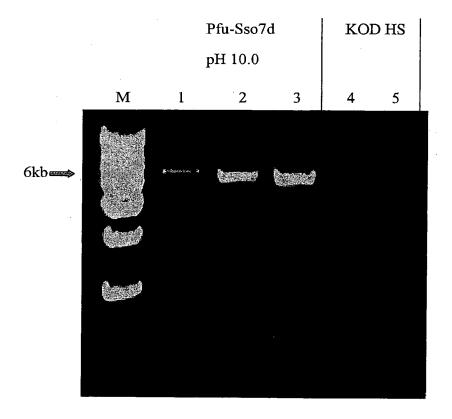
900bp HαAT 1"/kb - 1" extension



2.6kb HαAT 2"/kb - 5" extension



6kb BG 10"/kb - 1' extension



2.6kb HαAT 30"/kb - 1'. 18" extension

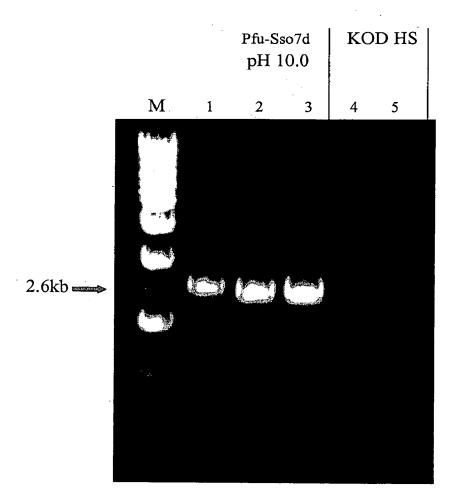


Figure 10. Oligonucleotide Primers for QuikChange Mutagenesis

V93E#1

5'-gAACATCCCCAAgATgAACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 5)

V93E#2

5'-CTTTTTCTCTAATAgTgggTTCATCTTgggggATgTTC-3' (SEQ ID NO: 6)

V93R#1

5'-gAACATCCCCAAgAT<u>AgA</u>CCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 7)

V93R#2

5'-CTTTTTCTCTAATAgTgggTCTATCTTgggggATgTTC-3' (SEQ ID NO: 8)

V93N#1

5'-gAACATCCCCAAgAT<u>AAC</u>CCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 9)

V93N#2

5'-CTTTTTCTCTAATAgTggggTTATCTTgggggATgTTC-3' (SEQ ID NO: 10)

V93H#1

5'-gAACATCCCCAAgAT<u>CAC</u>CCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 11)

V93H#2

5'-CTTTTTCTCTAATAgTggggTgATCTTgggggATgTTC-3' (SEQ ID NO: 12)

V93X (for saturation mutagenesis; obtained V93G and V93L mutants from library)

5'-(Phosphate)gAACATCCCCAAgATNNKCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 13)

V93K#1

5'-gAACATCCCCAAgAT<u>AAA</u>CCCACTATTAgAg-3' (SEQ ID NO: 14)

V93K#2

5'-CTCTAATAgTgggTTTATCTTgggggATgTTC-3' (SEQ ID NO: 15)

QCM#1 5'-(Phosphate)gAACATCCCCAAgATgCACCCACTATTAgAgAAAAAg-(SEQ ID NO:

16)'

Alanine

QCM#2 5'-(Phosphate)gAACATCCCCAAgATgACCCCACTATTAgAgAAAAAg-3'(SEQ ID

NO: 17)

Aspartic Acid

QCM#3 5'-(Phosphate)gAACATCCCCAAgATTgCCCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: 18)

Cysteine

QCM#4 5'-

(Phosphate)gAACATCCCCAAgATATACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 19)

Isoleucine

QCM#5 5'-(Phosphate)gAACATCCCCAAgATATgCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: 20)

Methionine

QCM#6 5'-(Phosphate)gAACATCCCCAAgATTTCCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: 21)

Phenylalanine

QCM#7 5'-(Phosphate)gAACATCCCCAAgATCCTCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: 22)

Proline

QCM#8 5'-(Phosphate)gAACATCCCCAAgATAgCCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: 23)

Serine

QCM#9 5'-(Phosphate)gAACATCCCCAAgATACACCCACTATTAgAgAAAAAg- 3' (SEQ ID

NO: 24)

Threonine

OCM#10 5'-(Phosphate)gAACATCCCCAAgATTACCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: 25)

Tyrosine

QCM#11 5'-(Phosphate)gAACATCCCCAAgATTggCCCACTATTAgAgAAAAAg-3'

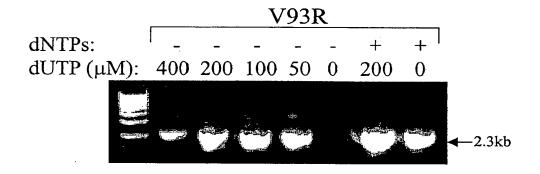
(SEQ ID NO: 26)

Tryptophan

a.)



b.)



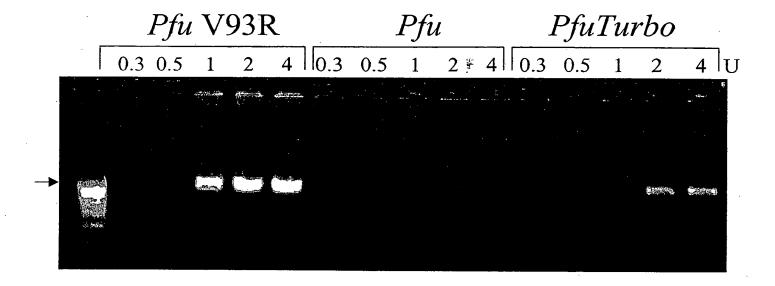


FIGURE 13A

PFU DNA POLYMERASE

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 27)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 28)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATMNNC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660 AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920 GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

PFU DNA POLYMERASE

FIGURE 13A (CONT.)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T) V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 29) V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATNNNC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540 GTTGAGGTTG TATCAAGCGA GAGAGAGTG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660 AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920 GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

PFU DNA POLYMERASE

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 31)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 32)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120

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CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATNNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGGTGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328
```

KOD DNA POLYMERASE

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 33)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 34)

ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACMNNC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780

FIGURE 13A (CONT.)

```
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTTGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CTTGA 2325
Vent DNA POLYMERASE
V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS
FOR ARGININE) (SEQ ID NO: 35)
V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO:
ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACNNNC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
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GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440 ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500

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GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325
Deep Vent
V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS
FOR ARGININE) (SEQ ID NO: 37)
V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO:
ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG
                                                                     60
AAAGAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT
                                                                    120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG
                                                                    180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACNNNC CCGCAATAAG GGATAAGATA
                                                                    300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC
                                                                    360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT
                                                                  420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA
                                                                    480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC
                                                                    540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG
                                                                    600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT
                                                                   720
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC
                                                                   780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG
                                                                    900
ACTGGAAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC
                                                                   960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG 1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC 1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA 1380
AGGCAAGAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT 1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC 1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA 1560
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA 1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC 1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG 1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA 1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG 1980
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CTAGTTATTT ACGAGCAGAT CACGAGGCCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC 2040
GTTGCCGTGG CAAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA 2100
GGGTACATAG TGCTGAGGGG AGACGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220

GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAGTAA 2328

JDF-3

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 39)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 40) ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGGACGGCGAGTTCA GGATTGAATACGACCGCGAGTTCGAGCCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAA GATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAAAAAGTTCCTCGGCAGGTCT GTGGAGGTCTGGGTCCTCTACTTCACGCACCCGCAGGACNNNCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGG TCATCGACATCTACGAGTACGACATACCCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGA GGAAGAGCTTAAACTCATGTCCTTCGACATCGACGCCTCTACCACGAGGGAGAAGAGTTTGGAACCGGGCCGATTCTG CCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATACAACGG GAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCA TAAGGCGCACCATAAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGT CTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAGAGGGTCGCGCGCTACTCGATGGAGGACGCG AGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGG CTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTACCCTTCAATCATAATCACCCACAACGTCTCGCCAGATA CATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTG GAGAAGAATCTCCTCGATTACAGGCAACGCGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATGCCA GGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGA GCTTGAGGAAAAGTTCGGTTTTAAAGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCT GAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCCTTCTCGAACTCGAATACG AGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCG CGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGCAGGCGAGGGTTTTGGAGGCGATACTCAGG CACGGTGACGTTGAAGAGGCCGTCAGAATTGTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGA AGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAGCG TTTGGCCGCCAGAGGTGTTAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGC GACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTC TGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGG GCTTGGCGCGTGGCTGAAGCCGAAGGGGAAGAAGAAGTGA

Figure 13B

>Pfu V93R (SEO ID NO:41)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS //

>Pfu V93E (SEQ ID NO:42)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93R/G387P (SEQ ID NO:43)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TPGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93R/D141A/E143A(SEQ ID NO:44)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFAIATLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93E/G387P(SEQ ID NO:45)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TPGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93E/D141A/E143A(SEQ ID NO:46)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFAIATLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>DEEP VENT V93R(SEQ ID NO:47)

MILDADYITEDGKPIIRIFKKENGEFKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAEKVRKKFLG
RPIEVWRLYFEHPQDRPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEAKVITWKKIDLPYVEVVSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSTGNLVEWYLLRKAYERNELAPNKPDEREYERRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLLKRLLDERQ
EIKRKMKASKDPIEKKMLDYRQRAIKILANSYYGYYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLEIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEEFDLRKHKYDAEYYIENQVLPAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
NIKKK

>DEEP VENT V93E (SEO ID NO:48)

MILDADYITEDGKPIIRIFKKENGEFKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAEKVRKKFLG
RPIEVWRLYFEHPQDEPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEAKVITWKKIDLPYVEVVSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSTGNLVEWYLLRKAYERNELAPNKPDEREYERRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLLKRLLDERQ
EIKRKMKASKDPIEKKMLDYRQRAIKILANSYYGYYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLEIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEEFDLRKHKYDAEYYIENQVLPAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
NIKKK

>TGO V93R (SEQ ID NO:49)

FIGURE 13B (CONT.)

MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
RPIEVWKLYFTHPQDRPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDLPYVDVVSTEKEMIKRFLKVVKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEEIAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLLGDLLEERQK
VKKKMKATIDPIEKKLLDYRQRAIKILANSFYGYYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLK

>TGO V93E(SEQ ID NO:50)

MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
RPIEVWKLYFTHPQDEPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDLPYVDVVSTEKEMIKRFLKVVKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEEIAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLLGDLLEERQK
VKKKMKATIDPIEKKLLDYRQRAIKILANSFYGYYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLK

>KOD V93R(SEQ ID NO:51)

MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDRPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPYVDVVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINFA
LGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAVFGQPKEKVYAEEITPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGYYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>KOD V93E(SEQ ID NO:52)

MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDEPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPYVDVVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINFA
LGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAVFGQPKEKVYAEEITPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGYYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

FIGURE 13B (CONT.)

>VENT V93R(SEO ID NO:53)

MILDTDYITKDGKPIIRIFKKENGEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGKTVRVLDAVKVRKKFLG
REVEVWKLIFEHPQDRPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIIMISYADEEEARVITWKNIDLPYVDVVSNEREMIKRFVQVVKEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEEIAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSILGDLIAM
RQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFYATIPGEKPELIKKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIHEQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYYIENQVLPAVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>VENT V93E(SEO ID NO:54)

MILDTDYITKDGKPIIRIFKKENGEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGKTVRVLDAVKVRKKFLG
REVEVWKLIFEHPQDEPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIIMISYADEEEARVITWKNIDLPYVDVVSNEREMIKRFVQVVKEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEEIAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSILGDLIAM
RQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFYATIPGEKPELIKKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIHEQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYYIENQVLPAVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>JDF-3 V93R(SEQ ID NO:55)

MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVKVKRAEKVKKKFLGR SVEVWVLYFTHPQDRPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGEEFGTGP ILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR DGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEEIATAWETGEGLERVARYS MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGGYAGGYVK EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLLGNLLEERQKIKRKMK ATLDPLEKNLLDYRQRAIKILANSYYGYYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLVIHEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI VLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

>JDF-3 V93E(SEQ ID NO:56)

MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVKVKRAEKVKKKFLGR SVEVWVLYFTHPQDEPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGEEFGTGP ILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR DGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEEIATAWETGEGLERVARYS MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGGYAGGYVK EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLLGNLLEERQKIKRKMK ATLDPLEKNLLDYRQRAIKILANSYYGYYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLVIHEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI VLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

Figure 14

Tgo 93:

NNN = AGA, AGG, CGA, CGC, CGG, CGT (R) (NUCLEOTIDE SEQUENCE: SEQ ID NO: 57; AMINO ACID SEQUENCE: SEQ ID NO: 58) NNN = GAA, GAG (E)(NUCLEOTIDE SEQUENCE: SEQ ID NO: 59; AMINO ACID SEQUENCE: SEQ ID NO: 60) atg atc ctc gat aca gac tac ata act gag gat gga aag ccc gtc atc 48 Met Ile Leu Asp Thr Asp Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile 96 agg atc ttc aag aag gag aac ggc gag ttc aaa ata gac tac gac aga Arq Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Asp Tyr Asp Arg aac ttt gag cca tac atc tac gcg ctc ttg aag gac gac tct gcg att 144 Asn Phe Glu Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile gag gac gtc aag aag ata act gcc gag agg cac ggc act acc gtt agg 192 Glu Asp Val Lys Lys Ile Thr Ala Glu Arg His Gly Thr Thr Val Arg 50 gtt gtc agg gcc gag aaa gtg aag aag ttc cta ggc agg ccg ata 240 Val Val Arg Ala Glu Lys Val Lys Lys Phe Leu Gly Arg Pro Ile 65 70 gag gtc tgg aag ctc tac ttc act cac ccc cag gac nnn ccc gca atc 288 Glu Val Trp Lys Leu Tyr Phe Thr His Pro Gln Asp Xaa Pro Ala Ile 85 agg gac aag ata aag gag cat cct gcc gtt gtg gac atc tac gag tac 336 Arg Asp Lys Ile Lys Glu His Pro Ala Val Val Asp Ile Tyr Glu Tyr 100 105 gac atc ccc ttc gcg aag cgc tac ctc ata gac aaa ggc tta atc ccg 384 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 120 atg gag ggc gac gag gaa ctt aag atg ctc gcc ttc gac atc gag acg 432 Met Glu Gly Asp Glu Glu Leu Lys Met Leu Ala Phe Asp Ile Glu Thr ctc tat cac gag ggc gag gag ttc gcc gaa ggg cct atc ctg atg ata 480 Leu Tyr His Glu Gly Glu Phe Ala Glu Gly Pro Ile Leu Met Ile 145 150 155 age tac gee gae gag gaa ggg geg ege gtt att ace tgg aag aat ate 528 Ser Tyr Ala Asp Glu Glu Gly Ala Arg Val Ile Thr Trp Lys Asn Ile 165 170 175 gac ctt ccc tat gtc gac gtc gtt tcc acc gag aag gag atg ata aag 576 Asp Leu Pro Tyr Val Asp Val Val Ser Thr Glu Lys Glu Met Ile Lys 180

FIGURE 14 (CONT.)

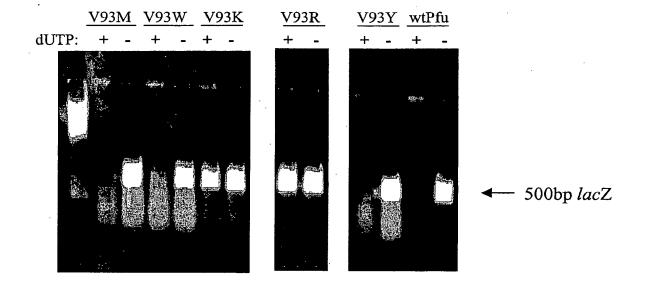
																•
_	ttc g Phe		_	_	-	_	-	_	_		-					624
	c aac c Asn 210		_			_		_			_	_	_			672
	g ctc s Leu 5															720
	c cag e Gln															768
	c ttc s Phe															816
	c acc r Thr															864
	g gtc s Val 290															912
	a gaa u Glu 5			_	_		_	_	_			_				960
_	a ctc ı Leu							_	_	_	_		_	_		1008
_	a ggc l Gly	_	_			_	_		_	_	_					1056
_	c gag l Glu			_	_		_						_		-	1104
	a aac o Asn 370	_	_	_			-	_								1152
	g ggt a Gly 5															1200
_	g tat l Tyr	_	_		-		_			_						1248
aa	c gtc	tcc	cct	gat	aca	ctc	aac	agg	gag	ggt	tgt	gag	gag	tac	gac	1296

FIGURE 14 (CONT.)

Asn	Val	Ser	Pro 420	Asp	Thr	Leu	Asn	Arg 425	Glu	Gly	Сув	Glu	Glu 430	Tyr	Asp	
					ggc Gly											1344
		_			gga Gly	_		_			_			_		1392
					act Thr 470											1440
					atc Ile											1488
					gcc Ala											1536
		_			agg Arg	_					_			_		1584
					ttt Phe											1632
					gga Gly 550											1680
_			_	_	tac Tyr			_		_			_		_	1728
					ttc Phe											1776
					gac Asp											1824
					gac Asp											1872
					ata Ile 630											1920
					gtt Val											1968

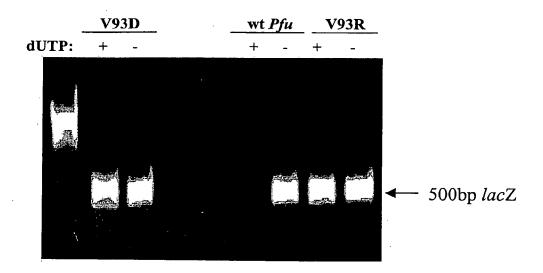
FIGURE 14 (CONT.)

	645	650	655
		g ata acc cgc gac ctg n Ile Thr Arg Asp Leu 5 670	Lys Asp
J J	JJJ J J J J	t gtt gca aaa cgc ctc a Val Ala Lys Arg Leu 685	•
		g gtc ata agc tac atc r Val Ile Ser Tyr Ile 700	
		g gct ata ccc ttt gac g Ala Ile Pro Phe Asp 715	
		a gaa tac tac atc gag a Glu Tyr Tyr Ile Glu 730	-
		g agg gcc ttt ggt tac u Arg Ala Phe Gly Tyr 5 750	Arg Lys
J J		g cag gtt ggc ttg ggg g Gln Val Gly Leu Gly 765	
cta aaa cct aag Leu Lys Pro Lys	_		2322



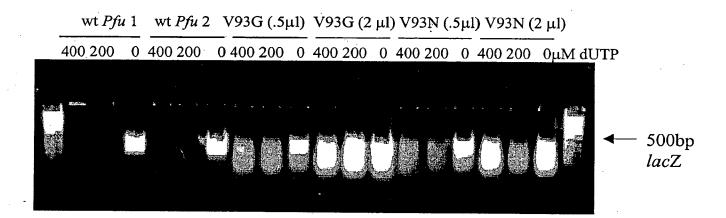
Results: *Pfu* V93K and V93R mutants show significantly improved dUTP incorporation compared to wild type *Pfu*. In contrast, the *Pfu* V93W, V93Y, and V93M mutants show little-to-no improvement in dUTP incorporation.

FIGURE 15B



Results: The Pfu V93D and V93R mutants show significantly improved dUTP incorporation compared to wild type Pfu.

FIGURE 15C



Results: The *Pfu* V93N mutant shows a very small improvement in dUTP incorporation compared to wild type *Pfu*. In contrast, the *Pfu* V93G mutant shows little-to-no improvement.

Figure 16: Polymerase activity and Temperature optimum of Pfu N terminal truncation mutants

Pfu clone #	Truncated after Pfu residue	Relative DNA polymerase activity	Temperature Optimum		
61	H30	Moderate	65°		
72	V66	Similar to wild type	70°		
81	P128	Low	Not tested		
92	I158	Low	Not tested		
3	G125	Similar to wild type	Not tested		
13/14	K201	low	65°		

Figure 17A

	18 54	36 108	54 162	69
	g GGT	E GAA	R AGA	
	A GCT	E	G GGT	
	K AAG	L	A GCA	
	R AGA	H	CAC	* TGA
al	I ATA	E	K AAG	s AGC
(HMf-like)	L	A GCA	A GCA	K AAG
HMÉ-	R AGA	r CTT	r CTT	I ATT
	D GAC	V GTA	D GAT	A GCA
histone	V GTT	K AAG	V GTA	L
	P CCA	A GCT	A GCA	K AAG
archaeal O: 63)	A GCC	A GCA	K AAG	I ATT
u zz	I ATT	cy v	K AAA	D GAC
G ID N	PCCA	EGAG	A GCA	E GAA
gene 3081) (SEQ (SEQ	L TTA	S AGC	I ATC	v GTC
furiosus No: AB013(sequence sequence	E GAA	V GTT	E GAG	K AAG
furiosus No: AB01. sequence	g GGA	R AGA	I ATT	V GTT
	M ATG	o CAG	A GCT	T ACC
Pyrococcus (ACCESSION Nucleotide Amino acid	M ATG	GCT	K AAA	K AAG

Figure 17B

(HMf-like)-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 65) Amino acid sequence (SEQ ID NO: 64) // Amino acid sequence (SEQ ID NO: 66)

18	36	54	69
54	108	162	
GGT	E	r Aga	
A GCT	E	g GGT	
K	L	A	
AAG	CTT	GCA	
r aga	H CAC	H	
I	E	K	s
ATA	GAG	AAG	AGC
L	A	A	K
CTT	GCA	GCA	AAG
r Aga	L	$_{ m L}$	I ATT
D	V	D	gca
GAC	GTA	GAT	Bca
V	K	V	r
GTT	AAG	GTA	CTC
P	A	A	K
CCA	GCT	GCA	AAG
A	A	K	I
GCC	GCA	AAG	ATT
I ATT	CAA	A A A	D GAC
PCCA	E GAG	A GCA	GAA
L	S	I	V
TTA	AGC	ATC	GTC
E	V	E	K
GAA	GTT	GAG	AAG
g	r	I	V
GGA	Aga	ATT	GTT
M	Q	A	T
ATG	CAG	GCT	ACC
M	A	K	K
ATG	GCT	AAA	AAG

6 6 6 6 GG GGC GGT

V GTG CTG CIC V GTC გ ე ရှိ ရ AAG . CCC GAG L F CTC TTT CCC crg M ATG S G AGT GGG P V T GTC ACT

ACC. ACC CIC ဗ္ဗဇ္ဗင A.A.G CTG A GCC H CAC \mathbf{r} T ACC R CGC Y A GCC \mathbf{r} CAC CAC ဝ ၁၅ GAC

K AAG r CTC CIC S AGC K AAG **₽** F ၁ ၁၅ Y TAC V GTC A GCG CAG V GTG CCG gag Gag ი მვვ R CGG S AGC မှ ည gg 🌣 K AAG A GCC GAC F V GTC V GTG I ATC V GTG A GCG D GAC ი მმ GAC E GAG K AAG CTC gcc Gcc

CCA T ACG P CCC CCC A GCC සි දි စ ဗ္ဗ A GCG K AAG Y ი მვვ ව වූ Y TAC A GCC E GAG CAC ස ප F

S

ი მმც CŢĠ r Si DGAC V GTG L CTG E GAG K AAG I ATC CIC gcc Bcc CIC o g සි රයියි CCC F TTT DGAC GAG

CTG s AGC A GCC L CTG V GTC DGAC D GAC A GCG E GAG Y TAC ဗ္ဗဗ္ဗ P CCG V GTC E CTC සි A GCG L CTG A A A DGAC A GCC T ACC CTC R I CGC ATC v GTC E GAG Y ဗ္ဗဋ္ဌ E GAG E K GAA AAG (A GCG K AAG K AAG GCC . Y ය ශීශීශී E GAG CCC H V L GTC CTC (H S D R I TCC GAC CGC ATC Q L L CAG CTC CTT Y TAC D L GAC CTT

W TGG CAG DGAC CCC CCC R AGG r CTG ဗဗ Y TAC W E K TGG GAA AAG L W gcc . P CCG T ACC IATC CTC /

K AAG GTC > ი წვ CCC Д r CTT AAC z GAC Ω S TCC GAG 闰 GAC Δ 999 Ö ₽ ACC CIG A GCC R CGG Y GAC gg A

GAA r CTG s AGC W TGG E E r CTG CIT K AAG R AGG A GCG T ACG AAG GAG ი გე I ATC

D GAC A r Eg 디디 A A GCC CTG A ဗ္ဗဗ္ဗ F සු පු V GTG L ATC I ATC ဗ္ဗဋ္ဌ ი მგმ CTG ₽ Ç AAA AAA V GTT R AGG CHC Y L Y E ၁ ဗိုင္ပ K AAG F TTC GAA r CTT Y TAT မှ ည GAG S AGC CTC မှ ၁ R AGG CTT ₽ PCG E GAG E E GAG V GTG සු පු P D GAT CCT r CTG M ATG CGG E ₩ TGG A G **₽** GGG GCC E A A B D GAC CAC විරියි GAC S TCC E GAG V GTG မှ ည် A GCC L I ATC ကို ည W TGG A GCC GCC CCC CTC CCC k AAA DGAC V GTG r CTT CIC M ATG E GAG **₽** M ATG r CTG E CTC ₩ TGG ₽ GCC A GCC DGAC ი მვვ A GCC R AGG CAC r CTG GGG D GAC CCC ය ලීලී S AGC မှ ည CGG CTC ဗ္ဗဗ္ဗ EGAG E A GCC S TCC A GCC K AAG w TGG R AGG g GGC A GCC E CAC r CTT GGC CGC R CGG r CTG GCC CCC E Γ r CTG န TCC K AAA F TTT E GAG A.A.G v GTC ი მვი P E ව පුර V GTC gcc ACC GGG R E GAG GGC CGC CGG CTC A GCC R CGG CIC T ACC E A GCT R AGG g GGG D GAC K AAG FTTC r CTG S TCC ය යි A GCG CIT င် အ AAC A GCG s TCC CTC r GTT CŢĞ D GAC R AGG A GCC CŢĠ r 'r CTT ය යියිය E GAG s TCC Y TAT $_{\rm CTT}^{\rm L}$ E GAG CTT R AGG AAC K AAG E GAG r Agg D GAT V GTG V GTG AAG ය ය PCCT EGAG ი გემ CCC GCC GCC K AAG DGAC EGAG r CTG မှ ငြင် F TTT A GCC L T ACG V GTG E GAA D GAC W TGG R AGG D GAC D M ATG L F TTT S AGC စ ဗ္ဗ A GCC R AGG CIG ¥ TGG r CTG E GAG r SEO CAC E GAA V GTG rg CG CG A GCC A GCC R AGG $_{
m L}^{
m L}$ CIC E GAG AAC AAC r CTG V GTG g G G gcc L CTG F r CTG CIC A GCC LCTG R AGG Y TAC ი შვც 3 3 3 3 4 E က္က ည်

FIGURE 17B (CONT.)

ACC Y TAT F N AAC I **A** 535 T ACG SAGT R AGG I ATC IATC **A** 225 F CC DGAC L M ATG ACC. r Cic A EGAG r CTC R AGG r TA Q SAC CTA F E မှ ည R GG ၁ ဗိုင္ပ r CTG N AAC ₩ TGG K AAG E AAC မှ ည r s AGC 9 9 9 9 CAC ဗ ဗ္ဗ CTT E S AGC F V GTC සි පි A GCC o CAG CTT မှ ည **₽** Y TAC I ATC ACG ტ ე V GTG DGAC ₽ GCC ₽ GCG s ICC ය ශීශීශී F A GCC CAG r CTC A GCC T ACC L TTG ရ ၁၉ T ACC ය දුව LCTC H r CTA Y CTA စ ဥ S AGC CTG DGAC ACG ဗ ပ္ပင္ပ s TCC ဗ္ဗ GAG GAG ဗ္ဗ မှု gg 🌣 D GAC T ACC I ATC ත් දි A GCC W r CTC TACG M ATG V 3TC CAC EGAG 闰 s TCC k AAG r TTG T ACG ი მვვ CAC CAC L A GCC r CTG F မှ ည I ATT Ы E A GCC GGC BBC E CCC P CAG I I ATC අ රි s TCG යියි CIC F E k AAG V GTG DGAC AAC N AAC L CTG GAC GAC M ATG F V GTC A GCC V GTC I ATC I ATT F CAG **₽** R AGG ရှိ ဗ V GTG CGG V GTG g GGC CAG CAG F I TTC ATC Y TAC CTC ი მმ GAG GAA T ACC ကို ည GG R R AGG A GCC Y TAC **₽** H, A.A.G T ACC N AAC r CTC E E GAG CIC GCC GCC r CTG CAC T ACC GAG 3 CAG CAG E GAG s AGC E A GCC H မှ ည A GCC CAG සි පි V GTC E GAG Ø K AAG CTC GAC T ACG E CIC DGAT CGG I ATA F က ည ი მმმ Y CAG GGC K AAG L န ၂၄၄ ය රි V GTC V GTC F සි දි rgC CGC အင္လ G P 3 3 3 5 5 CTC K AAG ဗ္ဗဋ္ဌ S AGC ဗ္ဗဋ္ဌ AAC AAC S ICC ဗ္ဗဋ္ဌ s AGC I ATC සි පි I

FIGURE 17B (CONT.)

V GTG R CGG CTG GAG GAG GGC AGG AGG CGG V E T L F G R R Y V P D L E A GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC ATT GAG AAG ACC AAG GTG CGG GCC TGG

g GGC CAG R E A A E R M A F N M P V CGG GAG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC V GTG K S AAG AGC (

E GAG r CTG A D L M K L A M V K L F P R GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG T A T A A ACC GCC (A GCC E M G A R M L L Q V H D E L V L E GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAG CTG GTC CTC GAG

ი მვვ E A E A V A R L A K E V M GCG GAG GCC CGG CTG GCC AAG GAG GTC ATG R AGG GAG P K CCA AAA

w TGG GAC V Y P L A V P L E V E V G I G E GTG TAT CCC CTG GCG CTG GAG GTG GGG ATA GGG GAG

CAT H L S A K E G I D G R G G G H H CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGG CAT CAT

H H * CAT CAT TAA

Figure 17C

Tag DNA polymerase- (HMf-like) fusion protein

Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 64) Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 63)

9 9 9 GGC GGC GGT

GTG V T S G M L P L F E P K G R V L L GTC ACT AGT GGG ATG CTC CTC TTT GAG CCC AAG GGC CGG GTC CTG

FIGURE 17C (CONT.)

- ဗ္ဗဗ္ဗ AAG L CTG A GCC CAC F T ACC යියි Y A GCC r CTG ය ය DGAC
- K AAG r Si r CIC s AGC K AAG GCC F TTC ဗ္ဗဇ္ဗ Y TAC V GTC A GCG CAG V GTG P CCG E ი წვ R CGG s AGC
- P CCC CCC **4** 200 K AAG A GCC DGAC F V GTC V GTG IATC V GTG A GCG DGAC ය ශ්රී GAC GAG K AAG CIC 3CC
- GCA P ACG H ကို ည gcc က ည် ဗ ည် A GCG K AAG Y စ စ္ပ ი გგ Y TAC A GCC E CAC အင္အင္တ F န ပြင်င
- ი მმც CIG r Ci DGAC V GTG CIG GAG K AAG IATC CHC A GCC L CTC CAA O CGG မှ ည FTT D E
- - r G န္ A GCC CTG V GTC DGAC GAC A GCG E GAG Y ဗ ဥ္ဌ ල වි V GTC E r CTC ဗ္ဗ A GCG $_{\rm L}^{\rm L}$
- X & GAC A GCC T ACC L R I CGC ATC V GTC E Y ဗ ဗ္ဗ E K AAG E A GCG K AAG K AAG A G
- Y ი წ E မှ ငြင်င CAC L V GTC CAC IATC CGC P DGAC s TCC r CIT CIC CAG Y TAC $_{
 m L}$ DGAC
- W CAG CAG DGAC r CCC R AGG L CTG GGC Y ·K AAG E GAA W L W A GCC P T IATC CTC
- K AAG GTC > ව පිරි ပိုင္ပင္ပ CIT N AAC D GAC / S E GAC ი მვვ T ACC L CTG A GCC ස දු TAC × GAC GCC GCC
- GAA L s AGC ი მვვ W TGG E GAG E GAG r CTG CIT K AAG R AGG A GCG TACG K AAG E GAG G GGG I ATC ဗ္ဗ
- GG I K AAG E ය ලීලී IATC A GCC က္ခ K AAG CIG ය රිපු D GAC r CTG AAC AAC K AAG CHO CTC 3 3 3 5 5
- GAC T ACC ය වි v GTG K AAG gcc r CTG DGAC W န TCC CIC K AAG CIG DGAT D GAC M ATG CAC A

FIGURE 17C (CONT.)

A **₽ A** 200 CIG A ရ ၁၉၅ I ATC CTT ı İİ F ۳ ک ک V GTG A AC V GTT CIC Y TAC E AGG ပ္ပင္ပ ව පු LCTG A AA Y FAC ი მმ L r G CTT F 3AA $\mathbf{r}^{\mathbf{Y}}$ CIC CTT E GAG N AAC GAC CGG GAG S AGC R R AGG T ACG 闰 D GAT TIC GAG P. CCG PCCT CIG M ATG ස උපි E ¥ ₹ A GCC **₽** ĮΞή E H A GCC DGAC CTT V GTG P CCG E GAG CCC A GCC s TCC မှ ည ය ශීශීශී L E CTG GAG M ATG k AAA D GAC V GTG H AGG CGG GAG CCC CTC r CCC W TGG P CCC CIT r CTC CAC M ATG r CTC W TGG A GCC A GCC GAC ი მვმ A GCC R AGG ဗ္ဗဗ္ဗ s AGC GCC r CCC R CGG CTC စ ဗိမ္မ E **₽** S A GCC E GAG gcc Bcc DGAC ဗ္ဗဗ္ဗ ₽ GCC E GAG CCC H LCTT မှ ၂ ය පු E r CTG r TTG L F TTT R K CGC AAG G L R A CTC AGG GCC ' F TTT E V GTC . GGG P T ACC E යියි GAC TTC GCC AAA ი მმმ V GTC 그닭 GAG E CIC F TTC (R CGG T ACC R CGG E GAG A GCT GTC စ ဗိုဗ္ဗ L CTT r CTG s TCC ය ය ი ენ N AAC S TCC A GCG ₽ GCG LCTT V GTC A Y GCC TAT R AGG A GCC r CTT CIT s TCC r CTT GAA ი მვვ E GAG E R AGG E E A GCC CTG GAG GTG K AAG V GTG R AGG K AAG CTG ဗ ဗ္ဗ PCCT E ი მმმ P CCC r CTG P CCC DGAC V GTG F TTT A GCC L CTG E GAA T ACG TGG R AGG GAG F TTT S AGC ဗ္ဗဗ္ဗ A GCC DGAC D GAC R AGG r CTG ₩ TGG L E GAG CTC D GAC E GAA A GCC V GTG CTG CCC A GCC R AGG L CTC E N AAC V GTG $_{
m L}$ က္က ည္ပ a G ი მმც A S F L CTG A GCC Y r CGC CTC E R AGG L A C

A GCC ACC. R GG Y TAT IATC F IATC A GG P Y F G S AGT org CAG CAG DGAC CIA r CTG M ATG ACC RGG LCTA F ц Б g GG က္ရ ဗ္ဗ CAG N AAC r CIG E မှ ည R AGG ი მმ CIG W K AAG E S AGC R CGG 4 S V GTC V GTC L CTT A GCC E s AGC සු පු H ဗ္ဗဗ္ဗ A GCC CAG CAG E P CCC CCC R AGG A GCC G C C C C Y I T V GTG GAC A GCC A GCG s TCC F TTT R AGG CIA MATG R T CGC ACC **4** CAG CAG CTC **A** L TTG ဗ ဗဗ္ဗ T ය දියි CIC Y ဗ္ဗဋ္ဌ D GAC AAC s AGC L S TCC E F CTG D GG R TACG CGC CGC R GGC EGAG CCA T ACC I ATC မှ ည **A** 325 V GTC W r CTC TACG MATG V GTG g GCC CAC E EGAG ာ သည် ව පුරි H CAC r CTG K AAG r Tr ACG P CCC A GCC Y TAC M ATG I ATT CIG E ₽ GCC IATC යියි CAG I ATC E မှ ည က ည F s TCG ය පු GG P ACC AAC ; K AAG V GTG AAC E L DGAC GAC DGAC M ATG **&** 9 K AAG င္ပင္သ GAG ၁၁၅ IATC I ATT F CAG A GCC V GTG R CGG V GTG ය ය O CAG E GAG GG R A GCC T ACC မှ ည cgc CGC r CTC I ATC R AGG ი ცვვ A GCC Y TAC Y TAC A GCC g GGC **₽** I ATT K AAG H T T ACC N AAC F r CTC E GAG E L E GAG E F ₩ IGG E GAG GCC CCC CAG ₽ GCC s AGC CAC A GCC E ය පු V GTC GG GG E GAG A 3CC r E K AAG D GAT ය විව I ATA F မှ သည Y TAC r G ი მვვ A G G V GTG R CGG සි වි S TCC යි දි CAG V GTC V GTC r GTG မှ ပိုင္ပ F CCT E s AGC V GTG ာ ဗဗ္ဗ r G AAG ဗ္ဗဋ္ဌ S AGC IATC S AGC ය වි ဗ္ဗဗ္ဗ IATC K AAG N AAC K AAG V GTG

FIGURE 17C (CONT.)

						18 54	36 108	54 162	69
EGAG	A GCC	9 999	W TGG	H CAT		GGT	E GAA	r Aga	
r CTG	E GAG	E GAG	D GAC	H CAT		A GCT	E	g GGT	
R AGG	CIC	M ATG	E GAG	H CAT		K AAG	CTT	A GCA	
P CCC	V GTC	v GTC	ი მიც	H CAT		r Aga	H	CAC	* TGA
F	CIG	E GAG	I ATA	ი ცვვ		I ATA	E GAG	K AAG	s AGC
LCTC	E	K AAG	ත ය	g GGC		CTT ;	A GCA	A GCA	K AAG
K AAG	DGAC	gg G	V GTG	GGA		r Aga	CTT	LCTT	I ATT
V GTG	Н	L CTG	E GAG	9 9		D GAC	v GTA	D GAT	A GCA
M ATG	V GTC	R CGG	V GTG	GGC		V GTT	K AAG	V GTA	CTC
A GCT	O CAG	gg G	E GAG	ဗ ဗဗ္ဗင		P CCA	A GCT	A GCA	K AAG
L CTG	L CTT	v GTG	$_{ m L}$	D GAT		A GCC	g A	K AAG	I ATT
K AAG	CTC	A GCC	P CCC	I ATT		I ATT	CAA	K AAA	D GAC
M ATG	M ATG	e gag	V GTG	ტ ცცე		P CCA	EGAG	A GCA	GAA
\mathbf{r}	R AGG	A GCG	A GCC	E GAG		L TTA	S AGC	I ATC	V GTC
DGAC	A GCC	R AGG	$_{ m CTG}$	K AAG		E GAA	V GTT	e Gag	K AAG
A GCC	ი მმ	E GAG	P CCC	A GCC	>>	G GGA	R AGA	I ATT	V GTT
A GCC	M ATG	K AAA	Y TAT	s TCC	H CAT	M ATG	OCAG	A GCT	T ACC
T ACC	E GAA	PCCA	V GTG	· CTC	H CAT	M ATG	A GCT	K AAA	K AAG

Figure 17D

Pfu DNA Polymerase (WT) -(HMf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 61) //Nucleotide sequence (SEQ ID NO: 63)

FIGURE 17D (CONT.)

ccetggtcct gggtccacat atatgttctt actcgccttt atgaagaatc ccccagtcgc totaacotgg gttatagtga caaaatottco tocaccacog cocaagaagg ttatttotat caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct aataccaatg gaggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaact tgggattaaa ttaaccattg gaagagatgg aagcgagcc aagatgcaga gaataggcga gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt

FIGURE 17D (CONT.)

tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta ttttattctt tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa gtagaagcgg cactactcag atgettecee aggaatgagg ttgttgtage tentecenga aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac aagattgaga tgttcttgg //

54 108 162 GAG CAC CTT GAG GAA AAG CAC GCA GGT AGA CTT ATA AGA AAG GCT GGT ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA AAG CAC AAA AAG GCA GTA GAT CTT GCA AAG CAC AAG ACC GTT AAG GTC GAA GAC TTA AAG AGC TGA

Figure 17E

(HMf-like) - Pfu DNA Polymerase (WT) fusion protein

Nucleotide sequence (SEQ ID NO: 63) //Nucleotide sequence (SEQ ID NO: 61)

54	108	162	
GGT	GAA	AGA	
GCT	GAG	gg	
AAG	CII	GCA	
AGA	CAC		<u> </u>
ATA	GAG	AAG	AGC
CTT	GCA	GCA	AAG
AGA	CIT	CIT	ATT
GAC	GTA	GAT	GCA
GTT		GTA	CIC
CCA	GCT	GCA	AAG
ggg	GCA	AAG	ATT
ATT		AAA	
CCA	GAG	GCA	GAA
TTA	AGC	ATC	GIC
GAA	GTT	GAG	AAG
GGA	AGA	ATT	\mathtt{GTT}
ATG	CAG	GCT	ACC
ATG	g_{CT}	AAA	AAG

ccctggtcct		gggtccacat atatgttctt actcgccttt atgaagaatc	actcgccttt	atgaagaatc	cccagtcgc
tctaacctgg	gttatagtga	caaatcttcc	caaatcttcc tccaccaccg	cccaagaagg	ttatttctat
caactctaca	cctcccctat	tttctctctt	atgagatttt	taagtatagt	tatagagaag
gttttatact	ccaaactgag	ttagtagata	tgtggggagc	ataatgattt	tagatgtgga
ttacataact	gaagaaggaa	aacctgttat	aacctgttat taggctattc	aaaaaagaga	acggaaaatt
taagatagag	catgatagaa	cttttagacc	atacatttac	gctcttctca	gggatgattc
aaagattgaa	gaagttaaga	aaataacggg	ggaaaggcat	ggaaagattg	tgagaattgt
tgatgtagag	aaggttgaga	aaaagtttct	cggcaagcct	attaccgtgt	ggaaacttta
tttggaacat	ccccaagatg	ccccaagatg ttcccactat	tagagaaaaa	gttagagaac	atccagcagt
gtggacatc	tgtggacatc ttcgaatacg atattccatt tgcaaagaga	atattccatt		tacctcatcg	acaaaggcct
aataccaatg	gagggggaag	aagagctaaa	aagagctaaa gattcttgcc ttcgatatag	ttcgatatag	aaaccctcta
tcacgaagga	gaagagtttg	gaagagtttg gaaaaggccc aattataatg attagttatg	aattataatg	attagttatg	cagatgaaaa
gaagcaaag	tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg	ggaaaaacat	agatcttcca	tacgttgagg	ttgtatcaag

FIGURE 17E (CONT.)

ttccggggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg tegtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag aggogatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt tttgctccaa gcagagccgc tccaatggat aacaccctg ttcccgcacc caagtccgct acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagagta gatgctacct aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta

FIGURE 17E (CONT.)

cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaact tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaagc gataaaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta ctgtaaggag tgtgctgaga gcgttactgc ctgggggaaga aagtacatcg agttagtatg gaaggagete gaagaaaagt ttggatttaa agteetetae attgaeaetg atggteteta tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac

FIGURE 17E (CONT.)

ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnn nngtcctctc ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa gtagaagcgg cactactcag atgettecee aggaatgagg ttgttgtage tentecenga TGA aagattgaga tgttcttgg //

Figure 17F

(HIMf-like) - PEU DNA POLYMERASE (V93 R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 27) Nucleotide sequence (SEQ ID NO: 63) //Nucleotide sequence (SEQ ID NO: 28) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

108 162 GCA GAG CAC CTT GAG GAA GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA CTT ATA AGA AAG GCT ATT AAG AGC // GAG CAA GCA GCT AAG GTA CTT CCA ATT GCC CCA GTT GAC AGA AAG ACC GIT AAG GIC GAA GAC AIT AAG CIC GCA TTA GCT CAG AGA GTT AGC AAA GCT ATT GAG ATC GAA ATG ATG GGA

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180 TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT AGAAAAAGTT CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT AAAGAGATAC TCTTGCCTTC TCTTCCATAC TATCAGGGAG ATATTAGCG AAAAACTIGG GATTAAATTA ACCATIGGAA GAGAIGGAAG CGAGCCCAAG ACCAATGGAG GGGGAAGAAG AGCTAAAGAT CCACTATTAG GGACATCTTC GAATACGATA TTCCATTTGC AAAACATAGA TTCTCAGGAT TACTIATAAT GGAGACTCAT TCGCATTCCC CAAGATXXXC AGCAAAGGTG ATTACTTGGA ATAAAGAGAT GAGAGAGATG GGAACATCCC ACATTATAGT AAGATIGIGA GAATIGITGA AACTTTATTT AAGGCCTAAT CAGCAGTTGT CCCTCTATCA ATGAAAATGA TATCAAGCGA AAAAGGGCAG ACCGTGTGGA AGAGAACATC CTCATCGACA GATATAGAAA AGTTATGCAG GTTGAGGTTG AAGGATCCTG

FIGURE 17F (CONT.)

1320 1500 1620 1680 1020 1080 1140 1200 1260 1380 1440 1560 1740 1800 1860 1920 1980 2040 2100 2160 TTTCGACTTG TGGACAACCT AGTAGGCCAC GGCAACTTAT ACTTAGGAAA GTTAGAGGAA AAAGAAAAG GCTTGAATAT TGTATATGAA TCAAAGAAGG GTGGGAAAAC TTATGGCTAT GGGAAGAAAG CCTCTACATT ACCAGAGAAG AGCTGAGGAA CAATGITTCI AATACTCCTT TGAAATTGCA TGAAGAAGCT AATGGTAATT ATACCAAAAG AGCCTGGGAA AATAGATGAA AGGTCCTCAC GAAGTCAAGG GAAGAATACA AGATAGCAAA AGTGGTTCTT CACTAGAGGC AAGATGCAAA CAAGATTAGT AAGAGGAGTA TAATTACCCA TCGCTCCTCA TGGGACATTT CTATAGAAAA TCTACGGATA TTACTGCCTG GATTTAAAGT GTGAGGAAAT GACTGCTAGA GGTATGCAGT GAGATTGGAG ACGGAGATGT ATGAAATTCC ATAAGGCGAT TAAAGCCAGG CGAIGGICCA ATTAGCAATA GGGCAATICT AAAAGGGGTT AAGACCTCAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // TACTCGATGG AACCTTGTAG AAGCCAAGTG AAAGAGCCAG TACAGAAAGG TACGCCGACG ATTCAGCTTT AACTATGATA GCTGAGAGCG AAGCTCCCTG ATACTAAAAC TTACATGAGT CCAACATACA CCCTCGATTA CCAAGTCTCT ACTCAAGATC GCAAATTCTT GAAAAGTTTG GGAGGAGAAA ATAGTTAGGA GGAGTTAAAA GAATATTACA ACGAAGAAGA CTTGCCAATT AAGCACAGGG GGGATGCAAG TTTGGAGACA TAGGCGATAT GACGGCTGTA AGTTGCCAAA TCCAATGGAA AGCTCCAAAC TGGTTTAGAG AGCTGCTAAA AATAAATCTC GGAGAAGGTA TGGATTCGTT AGCCCTATAT TGGTTTTATA AATGAAGGAA AAAACTCTTA TAAGGAGTGT GGAGCTCGAA AACTATCCCA CATAAATTCA ATTCTTCGTT AACAAGACCA GGGATTTGGA AATACAAAAG GTATGACGCA ATGAGCAGAT TAACAAGGAC ACCTTGAGAG AAGAATTCCT TTTCAAGGTC TAGATTTTAG TTAAGACAAA AAAAAGCGAT GATGGTACTG TAGTATGGAA GTCTCTATGC ATAAGAGGGG AAGCTAGAGT CAAAGAAACT GAAACGAAGT GCTACACAGG TAAATCTTGA AGGACATCCC TTGTAAAATA TAAAAGAAGT GAAAGCCAAA TCATTACTCG TACTTAGAGG AAAAGCACAA GGATATTGGA ACAAGACAAG ATGCAGAGAA AGTGGAGAGA GAACTCGGGA GACTATAGAC GCTCTAGAAT TACGATCCCA TATCATGTAA CCCGATACTC AGACAAAAGA GAAGGAAAAG CTCGCAATAT GCGCTACTTA GCAATTTTG TTATGGGATG ATAGTATACC AAGTTCTGCA GCAAAAGCAA TACATCGAGT GACACTGATG GAAGGGTTTT AAAGAAACTC GCCTACGAAA CTCAGGGAGA GTGAGAATAG GTAGCTGTTG GGATACATAG

Figure 17G

PFU DNA POLYMERASE (V93 R OR E)-(HIMf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 63)

FIGURE 17G (CONT.)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 1080 1140 1200 1260 1320 1380 1500 1620 1680 1800 1860 2100 1740 2040 1020 1440 1560 1920 1980 999 780 960 480 540 720 840 900 AAGGCATGGA CTGTTATTAG GCTATTCAAA CAAGCCTATT TATAATGATT TGTATATGAA TCAAAGAAGG GTGGGAAAAC AGTAGGCCAC GCTTGAATAT AATAGATGAA AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG TTAGACCATA CATTTACGCT AGAAAAGTT TCTTCCATAC TATCAGGGAG AGCCTGGGAA TGGACAACCT ACTTAGGAAA CAATGTTTCT GTTAGAGGAA AATACTCCTT TTATGGCTAT GGGAAGAAAG CCTCTACATT AAAGAAAAAG AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT AGGTCCTCAC TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA AAAGAGATAC TCTTGCCTTC ATATTTAGCG CGAGCCCAAG TTTCGACTTG GGCAACTTAT GAGATTGGAG TGAAATTGCA AGCTGAGGAA V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) GTTAAGAAA TAACGGGGGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CCACTATTAG TTCCATTTGC AGCTAAAGAT TTCTCAGGAT GAAGAATACA CACTAGAGGC AGATAGCAAA TCCAATGGAA ATTCAGCTTT CAAGATTAGT AAGCACAGGG AACCTTGTAG AGTGGTTCTT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA GGGATGCAAG AACTATGATA TCGCTCCTCA TGGGACATTT CTATAGAAAA TCTACGGATA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT GTGAGGAAAT GACTGCTAGA TAAAGCCAGG GGGCAATTCT AAGGCCCAAT GAGATGGAAG AAGATGCAAA TGGATTCGTT AAAGAGCCAG AAAAGGGGTT TAATTACCCA TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGTATGCAGT ATAAGGCGAT TCGCATTCCC ACCAATGGAG GGGGAAGAAG GAGTTTGGAA TACGCCGACG GAATACGATA GAAGGAAAAC GATAGAACTT GAAGTCAAGG CCAACATACA AGTTGCCAAA TACTCGATGG TGGTTTTATA CCAAGICTCT V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CAAGATXXXC ATAAAGAGAT GGAGACTCAT GATTAAATTA ACCATTGGAA GCAAATTCTT AACTATCCCA GGAGGAGAAA CATAAATTCA AAGCTCCCTG ACGAAGAAGA TGGTTTAGAG ATAGTTAGGA TTACATGAGT AGCTGCTAAA GGAGTTAAAA SGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA CCCTCGATTA AATGAAGGAA ACTCAAGATC ATGATTTTAG ATGTGGATTA CATAACTGAA AAAGAGAACG GAAAATTTAA GATAGAGCAT GACGGCTGTA AGCCCTATAT GATTGAAGAA GAGAGAGATG TACTTATAAT GGAGAAGGTA GGAACATCCC CGAAGGAGAA AAAACTCTTA ATTCTTCGTT GGACATCTTC AATAAATCTC AACAAGACCA TAACAAGGAC AAGAATTCCT GATGGTACTG ATGATTCAAA GAATTGTTGA TTTCAAGGTC AGGACATCCC TAGTATGGAA TAAAAGAAGT AACTTTATTT AAGGCCTAAT ATGAAAATGA AAAAACTTGG ACCTTGAGAG GAAACGAAGT TAGATTTTAG GTCTCTATGC CAGCAGTTGT CCCTCTATCA TAGGCGATAT GAAAGCCAAA GCTACACAGG TTAAGACAAA AAAAAGCGAT ATAAGAGGGG CAAAGAAACT TATCAAGCGA ACATTATAGT TAAATCTTGA TTGTAAAATA TCATTACTCG ATGAGCAGAT CTTCTCAGGG AAGATTGTGA GAACTCGGGA GTGAGAATAG ACCGTGTGGA AGAGAACATC CTCATCGACA GATATAGAAA ATGCAGAGAA AGTGGAGAGA TTATGGGATG GCCTACGAAA CTCAGGGAGA ATAGTATACC CCCGATACTC GACTATAGAC GACACTGATG GCTCTAGAAT AAAGAAACTC CTCGCAATAT GTAGCTGTTG AGTTATGCAG GTTGAGGTTG AAGGATCCTG AAAAGGGCAG TATCATGTAA GCAATTTTTG AAGTTCTGCA AGACAAAAGA GCAAAAGCAA TACATCGAGT GAAGGGTTTT GAAGGAAAAG

FIGURE 17G (CONT.)

	54	108	162	
2280 2328	ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT	GAA	AGA	
7G 22	GCI	GAG	GGI	
PAPA!	AAG	c_{II}	GCA	
ATACC	AGA	GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC	CAC	A C C
PAG 7	ATA	GAG	AAG	7
CCTC	CTT	GCA	GCA	AAG
AAGA AATC	AGA	CIT	CHI	ATT
AGG	GAC	GTA	GAT	400
AGAA ATTA	GTT	AAG	GTA	Į.
TAC	CCA	GCT	GCA	DAA
TGGA	ggg	GCA	AAG	₽ TT
GATT	ATT	CAA	AAA	SAC
A G	CCA	GAG	GCA	GAA
CTAP	TTA	AGC	ATC	GTC
GATA	GAA	GTT	GAG	AAG
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //	GGA	AGA	AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT	GTT
TACT	ATG	CAG	GCT	ACC
GCGG ACAA	ATG	GCT CAG	AAA	אסק אסר היים מרה היים מאם איים מאס מיים מאס מיים אסם אסם אסם אסם אסם אסם אסם אסם אסם אס

Figure 17H

PFU DNA POLYMERASE (G387P/V93R OR E) - (HMf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) or T) G387P Mutant (CCN is the codon for Proline where N = C, G, A, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

1020 1140 780 540 840 CACTAGAGGC TGTATATGAA CAAGATTAGT TGGACAACCT GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT TTTCGACTTG AGCCTGGGAA TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA SCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA CATTTACGCT GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT CCACTATTAG AGAAAAGTT AAAGAGATAC TCTTCCATAC TATCAGGGAG ATATTTAGCG CGAGCCCAAG GGCAACTTAT TTAGACCATA GGACATCTIC GAATACGATA TICCATITIGC AGCAAAGGTG ATTACTTGGA AAAACATAGA TTCTCAGGAT TCGCATTCCC GAGATGGAAG GAAGAATACA AGATAGCAAA AGTTGCCAAA TACTCGATGG AAGATGCAAA CCAACATACA GATAGAGCAT GATAGAACTT CAAGATXXXC GAGAGATG ATAAAGAGAT TACTTATAAT GGAGACTCAT GATTAAATTA ACCATTGGAA GACGGCTGTA GAAGTCAAGG TACGCCGACG GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT GGAACATCCC GGAGAAGGTA AATAAATCTC CAGCAGTTGT AAGGCCTAAT AACTTTATTT ATGAAAATGA TAACAAGGAC ACCTTGAGAG GAAAATTTAA ATGATTCAAA CCCTCTATCA TATCAAGCGA AAAAACTTGG TAGGCGATAT GAAAGCCAAA ACATTATAGT AAAGAGAACG AGTTATGCAG AAAAGGGCAG AAGATTGTGA ACCGTGTGGA AGAGAACATC CTCATCGACA GATATAGAAA AAGGATCCTG **TATCATGTAA** AGTGGAGAGA CTTCTCAGGG GTTGAGGTTG ATGCAGAGAA GCAATTTTG

FIGURE 17H (CONT.)

CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200	CCCTCGATTA TAATTACCCA CAATGTTTCT 1260	TGATA TCGCTCCTCA AGTAGGCCAC 1320	TCTCT TGGGACATTT GTTAGAGGAA 1380	AGATC CTATAGAAAA AATACTCCTT 1440	TTCTT TCTACGGATA TTATGGCTAT 1500	GAGCG TTACTGCCTG GGGAAGAAG 1560	GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620	GGAGGAGAAA GTGAGGAAAT AAAGAAAAG 1680	CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740	ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800	TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860	TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920	CITGCCAAIT AIGAAAIICC ACCAGAGAAG 1980	TGAGT ATAAGGCGAT AGGTCCTCAC 2040	GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100	CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160	TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220	TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280	ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
GAGCCAG AAAAGG	TCGATTA TAATTA	TATGATA TCGCTC	CCAAGTCTCT TGGGAC			GCTGAGAGCG TTACTG	AAGTTTG GATTTA	GGAGAAA GTGAGG	CTCCCTG GACTGC	AAGAAGA GGTATC	GTTAGGA GAGATI	CTAAAAC ACGGAG	GCCAATT ATGAAA	TTACATGAGT ATAAGG	GTTAAAA TAAAGC	AGCAATA GGGCAA	TATTACA TGGAGA	AGAAAGG AAGACC	ATTAAAA AATCC
MGGATTCGTT AAA		GGGATGCAAG AACTATGATA	TGGTTTTATA CCA	TTAAGACAAA AATGAAGGAA ACTCAAGATC	AAAAAGCGAT AAAACTCTTA GCAAATTCTT	TAAGGAGTGT GCT	GGAGCTCGAA GAA	AACTATCCCA GGA	CATAAATTCA AAG	ATTCTTCGTT ACG	TGGTTTAGAG ATA	TTTGGAGACA ATA	AATACAAAAG CTT	AACAAGACCA TTA	AGCTGCTAAA GGA	CGATGGTCCA ATT	STATGACGCA GAA	SGGATTTGGA TAC	TTCCTGGCTT AAC
GCTACACACC	TAGATTTTAG AGCCCTATAT	TAAATCTTGA (AGGACATCCC	TTAAGACAAA		GATGGTACTG TAAGGAGTGT	TAGTATGGAA (GTCTCTATGC AACTATCCCA	TTGTAAAATA	ATAAGAGGG	TCATTACTCG	AAGCTAGAGT '	TAAAAGAAGT AATACAAAAG	ATGAGCAGAT	CAAAGAAACT	TACTTAGAGG	AAAAGCACAA (GGATATTGGA GGGATTTGGA	TCGGCCTAAC
CTCAGGGAGA	ATAGTATACC	CCCGATACTC	AAGTTCTGCA	AGACAAAAGA	GACTATAGAC	GCAAAAGCAA	TACATCGAGT	GACACTGATG	GCTCTAGAAT	GAAGGGTTTT	GAAGGAAAAG	AAAGAAACTC	GTGAGAATAG	CTCGCAATAT	GTAGCTGTTG	GGATACATAG	TACGATCCCA	GCGGTACTTA	ACAAGACAAG

54 108 162 ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA AGG CAC CTT GAG GAA AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA AAG ACC GTT AAG GTC GAA ATT AAG ACC TTT AAG GTC GAA ATT AAG AGC TGA

Figure 171

(HMf-like) - PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 29) Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 30)

G387P Mutant (CCN is the codon for Proline where N=C, G, A, or T) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT

54

FIGURE 17I (CONT.)

GCA GAG CAC CTT GAG GAA GCA AAG CAC GCA GGT AGA GAA GAC ATT AAG CTC GCA ATT AAG AGC // GCA AAA AAG GCA GTA GAT CTT AAG GTA CTT CAA GCA GCT GAG AAA GCT ATT GAG ATC AAG ACC GIT AAG GIC GTT AGC CAG AGA GCT

108

1500 1020 1080 1140 1200 1260 1320 1380 1440 1560 1620 1680 1740 1800 1860 2100 //ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 1920 2040 840 960 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 CTICTCAGGG ATGATICAAA GATIGAAGAA GTIAAGAAAA TAACGGGGGA AAGGCATGGA 180 CAAGCCTATT AGAAAAGTT AAAGAGATAC TCTTGCCTTC TATAATGATT TCTTCCATAC TATCAGGGAG CGAGCCCAAG TTTCGACTTG TGTATATGAA AGCCTGGGAA GGCAACTTAT TGGACAACCT ACTTAGGAAA TCAAAGAAGG GTGGGAAAAC CAATGTTTCT TCGCTCCTCA AGTAGGCCAC GTTAGAGGAA TTATGGCTAT GGGAAGAAAG AAAGAAAAG GCTTGAATAT AATAGATGAA TGAAATTGCA AGGTCCTCAC AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA ATATTAGCG TGAAGAAGCT ACCAGAGAAG AATACTCCTT CCTCTACATT GTTGAGAAA AGTTTCTCGG CCACTATTAG GGACATCTTC GAATACGATA TTCCATTTGC ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TTCTCAGGAT AGTGGTTCTT GTGAGGAAAT GGTATGCAGT ATGAAATTCC GAGTTTGGAA AAGGCCCAAT TCGCATTCCC GAGATGGAAG GAAGAATACA AGATAGCAAA AAGATGCAAA CAAGATTAGT AAGAGGAGTA AAAAGGGGTT TAATTACCCA TCTACGGATA TTACTGCCTG ATAAGGCGAT AAAACATAGA CACTAGAGGC TGGGACATTT CTATAGAAAA GATTTAAAGT GACTGCTAGA GAGATTGGAG ATACTAAAAC ACGGAGATGT NGGATTCGTT AAAGAGCCAG GGAACATCCC CAAGATXXXC ATTACTTGGA TACGCCGACG TACTCGATGG CCCTCGATTA AACTATGATA GCAAATTCTT GCTGAGAGCG GGAGGAGAAA ATAGTTAGGA CTTGCCAATT ATAAAGAGAT GGAGACTCAT GATTAAATTA ACCATTGGAA GAAGTCAAGG CCAACATACA TCCAATGGAA ATTCAGCTTT AAGCACAGGG AACCTTGTAG AAGCCAAGTG CCAAGTCTCT ACTCAAGATC GAAAAGTTTG AAGCTCCCTG ACGAAGAAGA TTACATGAGT TGTAGAGAAG GGGATGCAAG ATTCTTCGTT CGAAGGAGAA AGCAAAGGTG GAGAGAGATG GACGGCTGTA GGAGAAGGTA AGTTGCCAAA AGCCCTATAT TGGTTTAGAG TTTGGAGACA TACTTATAAT AGCTCCAAAC TGGTTTTATA GGAGCTCGAA AACTATCCCA AATACAAAAG AATAAATCTC AATGAAGGAA AAAACTCTTA TAAGGAGTGT CATAAATTCA AACAAGACCA GAATTGTTGA AACTTTATTT CAGCAGTTGT AAGGCCTAAT CCCTCTATCA ATGAAAATGA TAACAAGGAC GAAAGCCAAA TTTCAAGGTC GCTACACACC AAAAAGCGAT ATAAGAGGGG TAAAAGAAGT CAAAGAAACT TATCAAGCGA ACATTATAGT AAAAACTTGG TAGGCGATAT ACCTTGAGAG AAGAATTCCT GAAACGAAGT TAGATTTTAG TAAATCTTGA AGGACATCCC TTAAGACAAA GATGGTACTG TAGTATGGAA GTCTCTATGC TTGTAAAATA TCATTACTCG AAGCTAGAGT ATGAGCAGAT TACTTAGAGG CTCATCGACA GTGAGAATAG ACCGTGTGGA GTTGAGGTTG AAGGATCCTG AGTGGAGAGA GAACTCGGGA CTCAGGGAGA GACTATAGAC GAAGGGTTTT AAAGAAACTC CTCGCAATAT AAGATTGTGA AGAGAACATC GATATAGAAA AGTTATGCAG AAAAGGGCAG ATGCAGAGAA TATCATGTAA GCAATTTTG TTATGGGATG GCCTACGAAA ATAGTATACC CCCGATACTC AAGTTCTGCA AGACAAAAGA GCAAAAGCAA TACATCGAGT GACACTGATG GCTCTAGAAT GAAGGAAAG GTAGCTGTTG GGATACATAG

FIGURE 17I (CONT.)

GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //TAG

Figure 17J

(HMF-LIKE) - PFU DNA POLYMERASE (D141A/E143A/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 31) Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 32)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG (ALL POSSIBLE CODONS FOR ARGININE) D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

108 162 GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC // TTA GAG ATC CAG AGA GIT AGC GAA ATG ATG GGA GCT ATT AAG ACC AAA GCT

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 9 ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180 600 AAAGAGATAC CAAGCCTATT TATAATGATT GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG ATATTTAGCG CGAGCCCAAG GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA AGAAAAGTT TCTTGCCTTC TCTTCCATAC TTTCGACTTG TGTATATGAA GGCAACTTAT TGGACAACCT CAGCAGTIGT GGACATCTIC GAATACGATA TICCATTIGC ACCAATGGAG GGGGAAGAAG AGCTAAAGAT AACTITATIT GGAACAICCC CAAGAIXXXC CCACTAITAG TCGCATTCCC TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG GAGATGGAAG CACTAGAGGC AGTIGCCAAA TACTCGAIGG AAGAIGCAAA CAAGATTAGT AAGGCCCAAT AAAACATAGA GAAGAATACA CGAAGGAGAA GAGTTTGGAA TCCAATGGAA ATTCAGCTTT ATTACTTGGA GGAGACTCAT ACCATTGGAA GAAGTCAAGG CCAACATACA TACTTATAAT GATTAAATTA AGCAAAGGTG AATAAATCTC GACGGCTGTA GAATTGTTGA AAGGCCTAAT ACCTTGAGAG CCCTCTATCA TATCAAGCGA ACATTATAGT AAAAACTTGG TAACAAGGAC GAAAGCCAAA AAGAATTCCT ATGAAAATGA TAGGCGATAT CTTCTCAGGG ACCGTGTGGA CTCATCGACA AAGGATCCTG ATGCAGAGAA AGTGGAGAGA SAACTCGGGA AAGATTGTGA GCNATAGCNA AGTTATGCAG GTTGAGGTTG AAAAGGGCAG **FATCATGTAA** SCAATTTTG AGAGAACATC

FIGURE 17J (CONT.)

GCTACACA GGT_GGATTCGTT AAAGAGCCAG AAAAGGGGGTT GTGGGAAAAC 1200 1740 TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080 GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 TAGATITIAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTITCT 1260 1440 1680 1800 1860 1920 1980 2040 2100 2160 1560 1620 2220 AGTAGGCCAC GTTAGAGGAA AATACTCCTT TTATGGCTAT CCTCTACATT AAAGAAAAG ACCAGAGAAG GGGAAGAAAG GCTTGAATAT TGAAATTGCA TGAAGAAGCT AGCTGAGGAA GGTTCTTCCA TACAGAAAGG AAGACCTCAG ATACCAAAAG AATAGATGAA AGGTCCTCAC AATGGTAATT CTATAGAAAA GGGATGCAAG AACTATGATA TCGCTCCTCA AGGACATCC TGGTTTTATA CCAAGTCTCT TGGGACATTT TCTACGGATA TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAGCTCGAA GAAAAGTTTG GATTTAAAGT GACTGCTAGA GGTATGCAGT TGGTTTAGAG ATAGTTAGGA GAGATTGGAG ACGGAGATGT ATGAAATTCC ATAAGGCGAT CGATGGTCCA ATTAGCAATA GGGCAATTCT GTATGACGCA GAATATTACA TGGAGAACCA GGAGGAGAAA GTGAGGAAAT TAAAGCCAGG TICCIGGUIT AACAITAAAA AAICC // ATACTAAAAC TTAAGACAAA AATGAAGGAA ACTCAAGATC AAGCTCCCTG CTTGCCAATT TTACATGAGT AGCTGCTAAA GGAGTTAAAA AAAACTCTTA GCAAATTCTT ACGAAGAAGA CATAAATTCA ATTCTTCGTT TTTGGAGACA AACTATCCCA AACAAGACCA GGGATTTGGA AATACAAAAG TCGGCCTAAC TAAATCTTGA GATGGTACTG TAGTATGGAA GTCTCTATGC AAAAGCGAT AAGCTAGAGT CAAAGAAACT ATAAGAGGG TCATTACTCG TAAAGAAGT ATGAGCAGAT TACTTAGAGG AAAAGCACAA GGATATTGGA TTGTAAAATA TTATGGGATG GGATACATAG ATAGTATACC GAAGGAAAAG CTCGCAATAT TACGATCCCA ACAAGACAAG GCCTACGAAA CTCAGGGAGA CCCGATACTC AAGTTCTGCA AGACAAAAGA GACTATAGAC GCAAAAGCAA GACACTGATG GCTCTAGAAT AAAGAAACTC STAGCTGTTG SCGGTACTTA TACATCGAGT GAAGGGTTTT GTGAGAATAG

TGA

Figure 17K

(HMF-LIKE) fusion protein PFU DNA POLYMERASE (D141A/E143A/V93R OR E)

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) G, A, or T) D141A/E143A Mutant (GCN is the codon for alanine where N = C, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT ATGATITIAG ATGIGGATIA CATAACIGAA GAAGGAAAAC CIGITATIAG GCTAIICAAA CATTIACGCT TTAGACCATA AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT CTTCTCAGGG ATGATTCAAA

FIGURE 17K (CONT.)

	TATCAGGGAG 600 ATATTTAGCG 660 CGAGCCCAAG 720 TTTCGACTTG 780 TGTATATGAA 840 AGCCTGGGAA 900	TGGACAACCT 1020 ACTTAGGAAA 1080 TCAAAGAAGG 1140 GTGGGAAAAC 1200 CAATGTTTCT 1260 AGTAGGCCAC 1320 GTTAGAGGAA 1380	AATACTCCTT 1440 TTATGGCTAT 1500 GGGAAGAAAG 1560 CCTCTACATT 1620 AAAGAAAAAG 1680 GCTTGAATAT 1740 AATAGATGAA 1860 TGAAATTGCA 1860 TGAAGAAGCT 1920 ACCAGAGAAG 1980 AGGTCCTCAC 2040 AATGGTAATT 2100 AATGGTAATT 2100 AATGGTAATT 2100 AATGGTAATT 2100 AATGCTAAAGA 2220 AATGCTAAAGA 2220 AATGCTAAAAG 2220 ATACCAAAAG 2280
	SAT TICTCAGGAT CAT TCGCATTCCC SAA GAGATGGAAG AGG GAAGAATACA ACA CACTAGAGGC ACA AGATAGCAAA TGG AGATAGCAAA	TTT CAAGATTAGT TAG AGTGGTTCTT STG AAGAGGGGTA CAG AAAGGGGTT TTA TAATTACCCA NTA TGGGACATTT TCT TGGGACATTT	
		A ATTCAGCTTT G AACCTTGTAG C AAGCCAGTG T AAAGAGCCAG T CCCTCGATTA G AACTATGATA A CCAAGTCTCT	
GGACATCTC GGACATCTTC ACCAATGGAG CGAAGGAGAA	GAGAGAGATG TACTTATAAT GATTAAATTA GACGGCTGTA AATAAATCTC GGAGAAGGTA	TCCAATGGAA AAGCACAGGG AGCTCCAAAC STGGATTCGTT AGCCCTATAT GGGATGCAAG TGGTTTTATA	AATGAAGGAA AAAACTCTTA TAAGGAGTGT GGAGCTCGAA AACTATCCCA ATTCTTCGTT TGGTTTAGAG TTTGGAGACA AATACAAAAG AACAGGACA AGCTGCTAAA GGATGTCCA GGGATTTGGA
AACITIAITI CAGCAGTTGT AAGGCCTAAT CCCTCTATCA	TATCAAGCGA ACATTATAGT AAAAACTTGG TAGGCGATAT TAAGACGAAA GAAAGCCAAA	AAGAATTCCT TCCAATGGAA TTTCAAGGTC AAGCACAGG GAAACGAAGT AGCTCCAAAC GCTACACA GGTGGATTCGTT TAGATTTTAG AGCCCTATAT TAAATCTTGA GGGATGCAAG AGGACATCCC TGGTTTTATA	TTAAGACAAA AAAAAGCGAT GATGGTACTG TAGTATGGAA GTCTCTATGC TTGTAAAATA ATAAGAGGGG AAAGCTAGAGT TAAAAGAACT TAAAAGAACT TAAAAGAACT TAAAAGAACT TAAAAGAACT TACTTAGGG AAAAGCACAA GGATATTGGA
ACCGTGTGGA AGAGAACATC CTCATCGACA GCNATAGCNA AGTTATGCAG	GTTGAGGTTG AAGGATCCTG AAAAGGGCAG ATGCAGAGAA TATCATGTAA GCAATTTTTG	GAACTCGGGA TTATGGGATG GCCTACGAAA CTCAGGGAGA ATAGTATACC CCCGATACTC AAGTTCTGCA	AGACAAAAGA GACTATAGAC GCAAAAGCAA TACATCGAGT GACACTGATG GACGCATTT GAAGGAAAAC GAAGGAAAAC GTGGCAATAT GTAGCATTG GTAGCTGTTG GGATACATAG GCGGTACCTAA ACGATCCCA

54 108 162 r ata aga aag gct ggt a gag cac ctt gag gaa a aag cac gca ggt aga a agc tga GCA GCA AAG CCA ATT GCC CCA GTT GAC AGA GAG CAA GCA GCT AAG GTA CTT GCA AAA AAG GCA GTA GAT CTT GAA GAC ATT AAG CTC GCA ATT GAA TTA GTT GTT GTT GTT GAG ATC GAG ATC AAG GTC GTC ATG ATG GGA GGCT CAG AGA GAAA GCT ATT GAAA GCT ATT GAAA GCT ATT GAAAA ACC GTT A

Figure 17L

KOD DNA POLYMERASE - (HMf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 63) CGT (ALL POSSIBLE CODONS FOR ARGININE) 1020 1140 1200 1260 1320 1440 1500 1080 900 99 840 900 960 CGTCTCGCCG AAGGGAGTAC CTGTCATAAG AATTTTCAAG CCTCAGGAAG GGCCAGAAGA CGGCCACCGC AGAGGAGAGG AAAGAAGGCT CTTCTACGCC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG GGACAAGATA CCTTATGATA CGTTTATGAA GGTCACATAC CGGCCAGTCC GGAGAACATA GCTCCTCGAT CGGCTATGCA CTACAGCGAC GAGACCAGTT CAAGCGCTAC GCTCGCCTTC TCTCCCCTAC TGTGAAGGAG CTATCTGAAA CGAGCCGAAG CTTCGATCTC AGCCTGGGAA GLUTAMIC ACID) TTGAACCCTA AGTTCCTCGG CAGCGATAAG TACCCTTCGC TCGACTTCGC AAATAACCAC AGTCGCCCGC TACTCGATGG AAGATGCGAA CTCGCTTAAT TCGAGAGGAA CGGCCTGGGG AAACCGTCAA AGCTGAAAAT AGAACGTGGA TCCTCCGTGT GGGATGGAAG GACGGATACA CGCTTGAGGC CAGCACTGGC AACCTCGTTG AGTGGTTCCT AAAAGGAGCT GAGGGTTGTG TCACCCACAA CCCCACAGGT GAGACCTCCT ACGGTTACTA TTAAGGTAAT GAGTICGCCG AGGGGCCAAT GCCGATGCTG ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC GGCGACAACT TCCGATGGAG GCCCAGCTTT AAGCCCGATG V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT GTTCAGAAGA GGCGACGAGG ATAACTTGGA GAAGTGAAGG CCCACATACA TACGCTGAGG TCAATCATCA TATGACGTTG AGCCTGCTTG ATTGACCCGA AACAGCTACT GAGAGCGTAA AAGTACGGCT V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CAGGACXXXC TGACATCTAC GAGTACGACA ATAAAGCGCT GCCCTCGGAA GAGCCCGAGA AACCTACAAC GGCCAGGGTG GGCCCCGAAC ATGCAAGGAA ATTTATCCCG GAAGGCCACG GATAGAGGAA GGTTGAAAG TGAGGGCGAG GAGGGAGATG AATAAACTTC CCTGTACCCC GATCCTGGCA GGAGTGTGCA AATACCTGGA GCCAATGGAA GTTTGCCGTC GGAGAAGGTT TACTCATCCG GATAAACCTG CTATGTAAAA TTTTTGCCAC CAGCAGTTAT AAAAGCTCGG ACCTTGAGAG ACAGAGAAGG ACTTCCCAGG AGAAGAAGAT AACTCTACTT CTCTCTACCA ACGAGGAAGG ACGTTCTCAT AGGAGTTCCT GGTACTGCAA CCATCAAGGA ACGATTCTGC CGGTTAAGCG AGGGATTAGT TCTCGACGGA TGGGCGACAG TAAGACGGAC GTCAGCCGAA TCTCCCGCTC GGAATGAGCT ATGAAGGAGG ATTTTAGATC GGGCCATCAA GTGTACCTAG TTCTGCAAGG CTCCTGAAGG GAGGTCTGGA GAGCTTGGGA CTCTGGGACG CGGCAGAGCT GATACGCTCA CAGAAGATAA ACGGTTGTAA GACATTGAAA AGCTACGCCG TATCCTGTGA GCCGTCTTCG ACCGGCGAGA GCCTATGAGA TACAGGCAGA AGGGCGCGCT ACCGACGGAT CGAGAGCATC CTCATAGACA GTTGACGTCG AAAGACCCGG AAGCGCTGTG ATTCAGAGGA ATAACGATGA

FIGURE 17L (CONT.)

ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740	C TC	AAGTAT	'AT C	AACGC	CAAA	CTT	ວອອອວວ	g CG	TTGA	GCT	CGAG	TACG	AG 1	740		
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGAA 1800	A AA	CGCGGC	LI	TTCG	CACG	AAG	AAGAAG	T AT	GGGI	GAT	AGAC	GAGG	7	800		
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860	A CA	ACGCGC	GG A	CTTG	GATT	GTG	AGGCGT	G AC	rggag	CGA	GATA	GCGA	4	860		
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG	G CG	AGGGTT	CTT	GAAGO	TTTG	CIA	AAGGAC	G GT	BACGI	CGA	GAAG	GCCG	13	1920		
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980	A AA	SAAGTT	'AC C	GAAA	AGCTG	AGO 1	AAGTAC	G AG	FITCO	ည္တင္သ	GGAG	AAGC	IG 1	980		
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040	G AG	CAGATA	AC G	AGGG7	TTTA	AAG	GACTAC	A AGO	SCAAC	CGG	TCCC	CACG	IT 2	040		
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100	A AG	AGGTTG	ပ္သင္သင္သ	GCGAG	AGGA	GIC	AAAATA	C GC	CTGG	AAC	GGTG	ATAA(32 2	100		
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160	CTC	AAGGGC	TC T	GGGAG	SGATA	999	GACAGG	G CG1	ATACC	GTT	CGAC	GAGT	IC 2	160		
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220	A AG(CACAAG	TAC	GACGC	CGAG	TAC	TACATT	G AG	AACCA	GGT	TCTC	CCAG	22 2	220		
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG	A TT(CTGAGA	ည	TTCGG	TTAC	S C C	AAGGAA	G AC	TGCG	CTA	CCAG	AAGA(3G 2	2280		
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT $2325/7$	G GT	TTGAGT	GC T	TGGCT	GAAG	ე ე	AAGGGA	A CT	232	ເດ						
ATG AT	G GG	A GAA	TTA	CCA 7	ATT G	S	ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT	GAC	AGA	CTT	ATA	AGA 1	AAG	GCT	GGT	54
GCT CA	CAG AG	A GTT	AGC	GAG C	AA G	CA G	AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG	GTA	CTT	GCA	GAG	CAC (CTT	GAG	GAA	108
AAA GCT	T AT	r GAG	ATC	GCA 7	AA A	AG G	ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA	GAT	CTT	GCA	AAG	CAC	3CA	GGT	AGA	162
AAG ACC GIT AAG	CGT	r AAG	GIC	GAA G	SAC A	TT A	GTC GAA GAC ATT AAG CTC GCA ATT	GCA	ATT	AAG	AAG AGC TGA	TGA				

Figure 17M

(HIMf-like) - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 33) Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 34) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

108 162 54 GCA GAG CAC CTT GAG GAA GCA AAG CAC GCA GGT AGA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC // CTT GAG CAA GCA GCT AAG GTA CTT GTA GAT ATT GAG ATC GCA AAA AAG GCA CCA GGA GAA TTA AGA GTT AGC ATG ATG GCT CAG AAA GCT

CTTCTACGCC 120 ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG GAGGCACGGG CAGCGATAAG GGACAAGATA CAGCAGITAI IGACAICTAC GAGIACGACA TACCCIICGC CAAGCGCIAC CICATAGACA AGGGATTAGI GCCAAIGGAA GGCGACGAGG AGCIGAAAAI GCICGCCIIC GAGACCAGTT TTGAACCCTA TAACCGCCGA AGTTCCTCGG GTTCAGAAGA GATTGAGTAC GACCGGACTT CATTGAGGAA GTCAAGAAGA TACTCATCCG CAGGACXXXC GGTTGAAAG GAGGTCTGGA AACTCTACTT GCGAGTTTAA ACGATTCTGC CGGTTAAGCG AAGGAAAACG CTCCTGAAGG CGAGAGCATC ACGGTTGTAA

FIGURE 17M (CONT.)

1200 1560 1020 1080 1140 1260 1320 1380 1440 1500 1620 1680 1740 1800 1860 1920 1980 2040 2100 2160 900 TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA CGGCCAGTCC TCTCCCCTAC CCTCAGGAAG TGTGAAGGAG CTTCGATCTC CGTTTATGAA AGCCTGGGAA GGTCACATAC GGAGAACATA CGTCTCGCCG CGGCTATGCA AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT CGAGTACGAG CGAGCCGAAG GGCCAGAAGA CGGCCACCGC AGAGGAGAGG GCTCCTCGAT AAGGGAGTAC CTACAGCGAC AGACGAGGAA GATAGCGAAA GGAGAAGCTG CGATACCGTT CGACGAGTTC CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG GAAGGCCGTG TCCCCACGIT GGTGATAAGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325 AGAACGTGGA CTCGCTTAAT GAGACCTCCT TTAAGGTAAT TCCTCCGTGT TCGACTTCGC GGGATGGAAG GACGGATACA CGCTTGAGGC AAATAACCAC AAGATGCGAA CAGCACTGGC AACCTCGTTG AGTGGTTCCT AAAAGGAGCT TCACCCACAA CCCCACAGGT TCGAGAGGAA ACGGTTACTA CGGCCTGGGG CGCTTGAGCT ATGCGGTGAT ACTIGAGATT GIGAGGCGTG ACTGGAGCGA CTAAAGGACG GTGACGTCGA GAGGGTTGTG AGGTTCCGCC AGGCAACCGG GCCCTGGAAC ATAACTTGGA GGCGACAACT TACGCTGAGG TACTCGATGG AAGCCCGATG ATTGACCCGA CCCACATACA GCCCAGCTTT TATGACGTTG TCAATCATCA ATTTATCCCG AGCCTGCTTG AACAGCTACT AAGTACGGCT AGCAAGTACG AAGGACTACA ATAAAGCGCT GCCCTCGGAA GAAGTGAAGG GAGCCCGAGA GAGAGCGTAA CTTCCGGGCG GGCGACAGGG AAGAAGAAGT GTCAAAATAC GGCCAGGGTG GAGGGAGATG TCCGATGGAG GAAGGCCACG GATCCTGGCA GATAGAGGAA AACCTACAAC AGTCGCCCGC GGCCCCGAAC ATGCAAGGAA GGAGTGTGCA GAGGGATTTA AATAAACTTC GTTTGCCGTC GATAAACCTG CTATGTAAAA CCTGTACCCC CAACGCCAAA CTTCGTCACG TGAAGCTTTG GGAGAAGGTT CGAAAAGCTG TGGGAGGATA CTTCGGTTAC CGCGAGAGGA CTCTCTACCA ACGAGGAAGG TCTCGACGGA ACGITCICAL AAAAGCTCGG TGGCCGACAG TAAGACGGAC ACCTTGAGAG AGGAGTTCCT GGAATGAGCT ACAGAGAAGG ACTTCCCAGG AGAAGAAGAT GTCAGCCGAA TCTCCCGCTC ATGAAGGAGG ATTTTAGATC GGGCCATCAA GGTACTGCAA CCATCAAGGA TTTTTGCCAC TCAAGTATAT AACGCGGCTT CAACGCGCGG AAGAAGTTAC AGAGGTTGGC AGCACAAGTA GTTTGAGTGC CGAGGGTTCT AGCAGATAAC TCAAGGGCTC TTCTGAGAGC GACATTGAAA AGCTACGCCG AAAGACCCGG ATTCAGAGGA CGGCAGAGCT GATACGCTCA TTCTGCAAGG GCCGTTGCCA TACATCGTGC GACCCGACGA GTTGACGTCG AAGCGCTGTG TATCCTGTGA SAGCTTGGGA CTCTGGGACG GCCTATGAGA GTGTACCTAG CAGAAGATAA TACAGGCAGA AGGCCCCCT ATAACGATGA ACCGACGGAT GGCAAGATAA GAGACGCAGG AGGATAGTCA GTGATCCACG STTGAGAGAA GCCGTCTTCG ACCGGCGAGA ATGGAGTTCC GGCTTCTACA AGACAGGTTG

Figure 17N

(HMf-like) - Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 36) Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 35)

FIGURE 17N (CONT.)

= AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) GAG (ALL CODONS FOR GLUTAMIC ACID) V93E MUTANT: XXX = GAA, V93R MUTANT: XXX

54	108	162	
GGT	GAA	AGA	
GCT	GAG	GGT	
AAG	CTT	GCA	
	CAC	CAC	/
ATA	GAG	AAG	AGC
CTT	GCA	GCA	AAG
AGA			
GAC	GTA		
		GTA	
CCA	GCT	GCA	
ggg	GCA	AAG	ATT
ATT	CAA	AAA	GAC
CCA	GAG	GCA	GAA
TTA	AGC	ATC	GIC
GAA	GLT	GAG	AAG
		ATT	GTT
ATG	CAG		ACC
	GCT		AAG

1200 1020 1080 1140 1260 1320 1380 1440 1500 1620 1560 1680 1740 480 540 900 099 720 780 840 900 960 300 GAGACATGGA AAGGGAAGTT GGGCAAAATA AATAATGATT TGAGGCAGTT GCTGATAGGT GTATCTTTTA AGAGTATAAA CGAAAAGAAA CGCATGGGGG CAAGCGTTAT CCTTGCCTTT TTTGCCGTAT GTATCTCATA AATCCACTTT TGCCGCTATA AGGTTTGTGG TAAGGTTCTT TTGGAGTGAG AATTTTAAG TATATATGCT ACATCCCGAA TGCTAGGGCA TACTCACAAC TCCGATAGTA GGACTTAATT CGGCTATATG ACTCATTAAA GCTTGAGCTT TGCAGTCATA TGTTAAAGAA TCAAGGGTAG CTGATGAGGA TAAAGGGCGA AATTTTGGG AGGGCGAGAT AAAAGCCTGA AACAAGGGGC TTGGAAGTAG TAAGGAGAGA CTATAATCCG CAGCTATGCG AGCTTAAGCT AAAATATCGA TTGATTTGCC GGGACAAAGA CAGAGGAAAT CAATGGAAGA AGCTGGCAAA TCGTGGAGTG AGCCAGAAAA ACGATGTTGC CCATACTCGG TTGACCCGAT ACAGCTATTA AAAGCGTTAC AGTICGGCTI TTCCAGGTCT AAAAGCGCTA TTCAGCCCTA TACCCTTTGC TTGTTCAAGT CGTATACGCT CAATAATAGT GATGGCAAGC TATTGAGGAG ATAAAGGCAA GGAGACGAGG GAATTTGGAA ATGGAAGCTG GAATGTGCTG ATAGAGGAAA ATACCCGGGG TTTGTTACAA GACCCTCATT GTCAGGAAAA CAAGACXXXC GAATATGACA ATCACATGGA GCTGTGGAAA AACCTCCCAA GCCCAGTACT ACCGGCAACC TATGTAAAAG AAATCCACAA TTGCTTGCAA AACTCCAAAC GGGGACAATT AAATTAGGAG CCGAACAAAC CTGTACCCTT TGTAAGAATT ATAAAGCGTT GTCTTAGGAA TTTATTCCCT CATAACAAAA GGCCAGAGTA AAGGACGATA ATTCTTCCCC GAGATCAAGC TTATGCCACA AAACTACATA TGACATTTAC TGAGGGAGAT AAGAGAAATG AACTTACAAT GTACTCGAAG GATAAGAGAA GAGAGGATTC AATAGAACTT TGCAGTGAAA CGAGCATCCC TCCCATGGAG AGTTCGGCTT AACCAAAAGC GAAAAAACTA TGAACTTGCA CCTGGGAGGA TTTCCGCAGT AAAAGAGGGC CTTTCCGGGC GAAGAAATG GGCTATTAAA TGATAGTTTT CAGTTGTGCG ATGACTCCGC TGTCCAATGA ATGTGATAAT AGGAATTCCT GCAGGATAAC ACACTGATTA GGGAGTTTAA GAGTGCTCGA AGCTCATTTT AGGCCTTGAT CGTTTTATCA ATGAAGAAGA AGAGGATGGG TTTTAGGAAA AAGAAAGCAT TCGGGAAGGA GGGACGTCTC ATACCCTTGA AGGCAAGATG CTGACGGCTT GCTTTTACTT CAGCTGTGGT AAAAGCTGGG ACGCGAGGAA GAACAACTTA TTTATTGGA TCTGCAAGGA AAGATATAAA ATAGGCAAAG TAGAGATGAC ATGATACTGG CTTCTCAAAG GATGAAGAGG TGGGAAACAG GTATCCCCAG AAGAAAGCCA GAAGTCTGGA GATATTGAAA AGGGTGGCAT GAAAATATCA GCAATGAGGC AGACACTACA TATGCGGACA AAAGAGAACG AAAACTGTGA CTCATAGACA AGTTATGCCG AAAGACCCCG AAACGGGCAG CCCAAGATTC GATCTTTTCC ACGTATGAGC CGGCGCTTAA GGATATAGGT GGGTATCCTA GAGTATGAGG AGGGAACATC GTCGATGTTG TATGAAGCAG CAAAGTGTAT ATGCTCGATT

FIGURE 17N (CONT.)

2160 2100 2220 2280 1980 2040 GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920 AATTTTACTT AAACCAAGTT TTTAAGGTAT GGTTCCACTT ACCGGGCACA AGCCATTGGC CAAAATACAG GCAAGAGGGA TAAAAGTGAA ACTACATAGA AGGACTACAA GCGATAGGGT GAAAGGAGGA CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325 GAGAAAATAG GGAAAGATAA GATCCGGACT TTTGGATACA AGGGATTTAA ATAGCTAAGG AGACTCAGGC AAAGGTTTTA CGATAGCAAA AAGACTTGCC TACTTAGGAT ACTCGAAGCG AGATGTTGTA GCAGATTACC CAAAGGGAGC ACACAAGTAC AAGTTGTTAG ATCCTAGAAA TTATCCATGA ATATCGTTCT ATAATAAGCT AAAGCTGTAG GAAAAGCTTG CCTCATGTCG ACAGAATACG TTGCCGGCAG

Figure 170

Vent DNA POLYMERASE - (HMf-like) FUSION PROTEIN

// Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 36) Nucleotide sequence (SEQ ID NO: 35)

CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) CGA, CGC, CGG, V93R MUTANT: XXX = AGA, AGG,

1020 1140 1200 9 840 900 CTATAATCCG AATTTTTAAG GAGACATGGA AATAATGATT GGGCAAAATA CAAGCGTTAT CCTTGCCTTT TGAGGCAGTT TGCTAGGGCA GCTGATAGGT TATATACT AAGGGAAGTT TTTGCCGTAT ACATCCCGAA AATCCACTTT TGCCGCTATA AGAGTATAAA AGCCAGAAAA AGGTTTGTGG TGTTAAAGAA GTATCTCATA TTCAGCCCTA AGGCCGAGAT TAAAGGGCGA AATTTTGGG TACCCTTTGC AAAATATCGA TTGTTCAAGT GGGACAAAGA TCAAGGGTAG CGTATACGCT CAGAGGAAAT CAATGGAAGA AGCTGGCAAA CAGCTATGCG AGCTTAAGCT TTGATTTGCC TCGTGGAGTG CTGATGAGGA GATGGCAAGC ATAAAGGCAA GGAGACGAGG GAATTTGGAA TATGTAAAAG GACCCTCATT GTCAGGAAAA GAATATGACA ATCACATGGA ATGGAAGCTG CAAGACXXXC GGGGACAATT GTCTTAGGAA GCTGTGGAAA AACCTCCCAA AAATTAGGAG ACCGGCAACC ATAAAGCGTT GCCCAGTACT CCGAACAAAC ACACTGATTA CATAACAAAA TATTGAGGAG CGAGCATCCC TGACATTTAC GGCCAGAGTA AACCAAAAGC ATTCTTCCCC CCTGGGAGGA AATAGAACTT TGCAGTGAAA TCCCATGGAG TGAGGGAGAT AAGAGAAATG AACTTACAAT AAGGACGATA GAAAAAACTA GAGATCAAGC TGATAGTTT TGAACTTGCA AGTICGGCTT GGGAGTTTAA ATGACTCCGC ATGTGATAAT TCGGGAAGGA GAGTGCTCGA CAGCTGTGGT AGGGCTTGAT CGTTTTATCA ATGAAGAAGA TGTCCAATGA AAAAGCTGGG AGAGGATGGG CAGTTGTGCG TTTAGGAAA AGCTCATTT GGGACGTCTC ACGCGAGGAA GAACAACTTA AAGAAAGCAT ATGATACTGG CTTCTCAAAG AAAGAGAACG AAAGACCCCG TGGGAAACAG AGGGTGGCAT GAAGTCTGGA AGGGAACATC CTCATAGACA GATATTGAAA AGTTATGCCG AAACGGGCAG CCCAAGATTC TATGAAGCAG CAAAGTGTAT CGGCGCTTAA AAAACTGTGA GTCGATGTTG GATCTTTCC ACGTATGAGC

FIGURE 170 (CONT.)

1320	1380	1440	1500	1560	1620	1680	1740	1800	1860	1920	1980	2040	2100	2160	2220	2280	
TCCGATAGTA 13	GGACTTAATT 13	CGAAAAGAAA 14	CGGCTATATG 1	CGCATGGGGG 1	TAAGGTTCTT 16												
ACGATGTTGC	TTTATTCCCT CCATACTCGG	TTGACCCGAT	ACAGCTATTA	GTACTCGAAG GAATGTGCTG AAAGCGTTAC	AGTTCGGCTT	TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA	AAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT	TITGITACAA AAAAGCGCTA IGCAGICAIA	GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG	ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA	AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT	TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC	CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA	ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT	ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT	TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT	GG 2325 //
TGTAAGAATT		AAATCCACAA	GGCTATTAAA TTGCTTGCAA ACAGCTATTA	GAATGTGCTG	GATAAGAGAA ATAGAGGAAA AGTTCGGCTT	ATACCCGGGG	AACTCCAAAC	TTTGTTACAA	TTGGAAGTAG	GAGGCTATAC	GAGAAAATAG	AGGGATTTAA	GCAAGAGGGA	GGAAAGATAA	GATCCGGACT	TTTGGATACA	CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //
ATACCCTTGA AAAAGAGGGC	CTTTCCGGGC	AAGATATAAA GAAGAAATG	GGCTATTAAA		GATAAGAGAA			GAGAGGATTC	AACAAGGGGC	AAAGGTTTTA	AGATGTTGTA	GCAGATTACC	AAGACTTGCC	CAAAGGGAGC	ACACAAGTAC	ACTCGAAGCG	CTTAGATGCA
ATACCCTTGA	TCTGCAAGGA	AAGATATAAA	ATAGGCAAAG	AGGCAAGATG	TAGAGATGAC	CTGACGGCTT	AAGAAAGCCA AGGAATTCCT	GCTTTTACTT		AGACTCAGGC	AAGTTGTTAG	TTATCCATGA	CGATAGCAAA	ATATCGTTCT	ATCCTAGAAA	TACTTAGGAT	AACAAACCGG
GTATCCCCAG	GGATATAGGT	GCAATGAGGC	ATGCTCGATT	GGGTATCCTA	AGACACTACA	TATGCGGACA	AAGAAAGCCA	GAGTATGAGG	GATGAAGAGG	ATAGCTAAGG	AAAGCTGTAG	GAAAAGCTTG	CCTCATGTCG	ATAATAAGCT	ACAGAATACG	TTGCCGGCAG	CAAAGCTCAA

108 162 GCA GAG CAC CTT GAG GAA GCA AAG CAC GCA GGT AGA CTT ATA AGA AAG GCT GGT GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC AAG ACC GTT AAG GTC GAA GAC ATT AAG TC GCA ATT AAG AGC TGA CCA ATT GCC CCA GTT GAC AGA TTA GAA ATG ATG GGA

Figure 17P

Deep Vent- (HMf-like) DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 63) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) 180 240 300 ATGATACTIG ACGCIGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG CCGCAATAAG GGATAAGATA AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC TIAGACCITA CATITACGCI AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT

FIGURE 17P (CONT.)

420	540	009	9	720	780	840	900	960	1020	1080	1140	1200	1260	1320	1380	1440	1500	1560	1620	1680	1740	1800	1860	1920	1980	2040	2100	2160	2220	2280	2328
GCTCGCATTT	TCTCCCGTAC	GATAAGGGAG	CTATCTAGTT	TGAGCCAAAG	CTTTGACCTC	AGTTTATGAG	GGCCTGGGAG	GGTAACGTAC	CGGCCAGCCC	CCTCAGGAAG	CGAGAGAAGG	CTGGGAGGGG	TAACGTCTCA	GGTTGGGCAC	ATTGGATGAA	GAAGATGCTT	TTATGGGTAC	GGGGAGGGAA	CTTATACATA	AAAGAAGAAA	GCTTGAGTAC	GATAGATGAG	CGAAATAGCC	TGAGGAGGCA	TCCAGAAAAG	AGGTCCGCAC	CATGGTGATA	TGCAGAGGAG	GGTTTTACCT	GTGGCAGAAG	
AGGGGCCCAT	AAAAGATCGA	TCCTCAAGGT	TCGACCTTCC	GGGACGGTAG	GAAGGATACA	CCCTCGAGGC	AGATAGCTGA	AGGATGCAAA	CAAGGTTAGT	AGTGGTACCT	AGAGGGAGTA	AGAAAGGGCT	TAATCACCCA	TCGCCCCAGA	TCAAGAGGTT	CAATCGAGAA	ATTATGGGTA	TTACGGCCTG	GGTTCAAAGT	CCGAGGAGAT	GGCTGTTGGA	AGTATGCGTT	GGGACTGGAG	ATGGCAACGT	ACGAAATACC	ACAAGGCTAT	TGAGGCCTGG	GGGCTATCCT	TAGAAAATCA	AAGACCTCAG	AGAAG //
GGCGATGAAG	ATAACGTGGA	ATAAAGCGGT	GGCGATICTI	CCCCTGGGAA	GAGATAAAGG	CCAACATACA	TACGCTCACG	TATTCAATGG	GCCCAGCTTT	AACTTGGTGG	AAGCCGGATG	AAGGAGCCGG	CCCTCGATAA	GAATACGATG	CCCAGCCTGC	TCTAAAGACC	GCAAACAGCT	GCAGAGAGCG	GAAAAGTTCG	GGGCCAAAAC	AAGCTCCCAG	ACGAAGAAGA	ATAGTCAGGA	ATCCTAAAGC	CTGAGCAAGT	CTTCACGAGT	GGAGTAAAGG	ATAAGCAAGA	GAGTATTACA	TACAGGAAAG	AACATCAAGA
TCCAATGGAA	AGCCAAAGTC	GAGGGAGATG	TACCTACAAC	GATAAAGCTA	GACAGCGGTG	GATAAACCTC	GGAGAAAGTT	AGTTGCAAAG	CCCAATGGAG	TTCAACTGGC	GGCTCCAAAC	GGGATACGTT	GAGCCTGTAC	AGGGTGTAGG	GGGGTTTATC	GATGAAAGCT	CAAAATCCTG	TAAGGAGTGC	GGAACTGGAG	CACAATTCCT	TATAAACGCC	GTTCTTCGTG	GGGGCTTGAA	CCTAGAGGCT	AACTGAAAAG	CACGAGGCCC	AGCCGCTAGA	AGACGGGCCA	GTATGACGCT	GGCCTTTGGG	GGCATGGCTT
AAGGCCTAAT	ATGAGGAAGA	TTTCCAGCGA	ATGTTATAAT	AAAAGCTCGG	TTGGGGATAT	TTAGGAGAAC	GAAAGCCAAA	GACTGGAGAG	GGGAGTTCTT	TTTCTAGGTC	GGAATGAATT	GCTACGCTGG	TAGATTTCAG	TGAACAGGGA	AGGACTTCCC	TAAAAAGGAA	AACGGGCAAT	GTTGGTACTG	TCGTAAGGAA	GACTCTACGC	TCGTAGATTA	ACGTGAGAGG	TAATCACTAG	AAGCAAAAGT	TTAAGGAGGT	ACGAGCAGAT	CAAAAAGGTT	TGCTGAGGGG	GGAAGCATAA	GAATATTAGA	CAGGTCTTAC
CTAATAGACA GACATAGAAA	AGCTATGCTG	GTCGAGGTAG	AAAGATCCCG	AAGAGGGCCG	ATGCAGAGGC	TACCACGTGA	GCAATCTTCG	ACTGGAAAGG	GAGCTCGGTA	CTGTGGGATG	GCCTACGAGA	CTAAGGGAGA	TTAGTTTCCC	CCGGATACGC	AAGTTCTGCA	AGGCAAGAAA	GATTACAGGC	GCAAAAGCCC	TATATAGAGT	GACACAGATG	GCCCTAGAGT	GAGGGCTTCT	GAAGGGAAGA	AAAGAAACCC	GTAAAGATAG	CTAGTTATTT	GTIGCCGIGG	GGGTACATAG	TTCGATCTCA	GCCGTTCTTA	ACTAAACAGA

54 108 162 ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT GCT CAG AGA GTT AGC GAG CAA GCT AAG GTA CTT GCA AAG GCT GAG GAA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA AAG ACC GTT AAG GTC GAA ATT AAG GTC GCA ATT AAG AGC TGA

FIGURE 17Q

(HMflike) - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 38) Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 37)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

108 162 GAG GAA GCA AAG CAC GCA GGT AGA CIT ATA AGA AAG GCT GCA GAG CAC CTT GAC ATT AAG CTC GCA ATT AAG AGC TGA GCA AAA AAG GCA GTA GAT CTT CCA GIT GAC AGA CAA GCA GCT AAG GTA CTT ATT GCC CCA GAG GAA TTA CAG AGA GTT AGC AAA GCT ATT GAG ATC AAG ACC GTT AAG GTC GAA GGA ATG GCT ATG

600 99 900 180 240 300 420 480 540 720 780 840 1020 1080 1140 1200 1380 360 960 1260 1320 1500 1440 ATGATACTIG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG TGAGCCAAAG AGTTTATGAG GCAGAGAGCG TTACGGCCTG GGGGAGGGAA GATAAGGGAG GGCCTGGGAG CCTCAGGAAG CGAGAGAAGG TAACGTCTCA GAGGCATGGG GAAGAGGTAC TATAATGATA TCTCCCGTAC CTTTGACCTC GGTAACGTAC CGGCCAGCCC CTGGGAGGGG GGTTGGGCAC CATTTACGCT GGATAAGATA GCTCGCATTT CTATCTAGTT ATTGGATGAA GAAGATGCTT TTAGACCTTA GATTGATGAG GTTAGGAAGA TAACCGCCGA TCCTCAAGGT GGGACGGTAG CCCTCGAGGC TCGCCCCAGA GTAAGGAAGA AGTTCCTGGG CCGCAATAAG GAGTICGCGA AGGGGCCCAT AAAAGATCGA GAAGGATACA AGATAGCTGA AGGATGCAAA AGAGGGAGTA TAATCACCCA TCAAGAGGTT TTCCGTTCGC GGCGATGAAG AGCTCAAGTT TCGACCTTCC CAAGGTTAGT AGTGGTACCT AGAAAGGGCT CAATCGAGAA ATTATGGGTA GGTTGAGTAC GACAGAAACT TACGCTCACG TATTCAATGG AAGCCGGATG AAGGAGCCGG CAGGACXXXC GAGTACGACA ATAACGTGGA CCCCTGGGAA CCAACATACA GAATACGATG ATAAAGCGGT GGCGATTCTT GAGATAAAGG GCCCAGCTTT AACTTGGTGG CCCTCGATAA CCCAGCCTGC TCTAAAGACC GCAAACAGCT AGTTGCAAAG TGCCGAAAAG GAGGGAGATG GATAAAGCTA GATAAACCTC GGAGAAAGTT TTCAACTGGC GGCTCCAAAC GGGATACGTT AGGCTGTAGG GATGAAAGCT GTTGGTACTG TAAGGAGTGC TGAACACCCT TGACATCTTT TCCAATGGAA AGCCAAAGTC TACCTACAAC GACAGCGGTG CCCAATGGAG GAGCCTGTAC CAAAATCCTG CGAAGGGGAG GGGGTTTATC GCGAGTTTAA ATGACTCGCA GAATTATAGA GGCTGTACTT CCGCAGTTAT AAGGCCTAAT CCCTCTATCA AAAAGCTCGG TTGGGGATAT TTAGGAGAAC GAAAGCCAAA GACTGGAGAG GGAATGAATT GCTACGCTGG TGAACAGGGA AGGACTTCCC ATGAGGAAGA TTTCCAGCGA ATGTTATAAT GGGAGTTCTT TTTCTAGGTC TAGATTTCAG TAAAAAGGAA AACGGGCAAT CTCCTCAAAG GATTACAGGC AAGATAGTGA AGCTATGCTG AAAGATCCCG GCAAAAGCCC AAAGAAAACG GTCGAGGTAG AAGAGGCCG TACCACGTGA GCCTACGAGA CTAAGGGAGA TTAGTTTCCC CCGGATACGC AAGTTCTGCA AGGCAAGAAA GAGGTATGGA AGAGAGCATT CTAATAGACA GACATAGAAA ATGCAGAGGC GCAATCTTCG ACTGGAAAGG SAGCTCGGTA CTGTGGGATG

FIGURE 17Q (CONT.)

1620	1680	1740	1800	1860	1920	1980	2040	2100	2160	2220	2280	2328
					•							.,
GGTTCAAAGT	GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA	GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC	GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG	GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC	AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA	GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG	CTAGTTATTT ACGAGCAGAT CACGAGGCCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC	GTTGCCGTGG CAAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA	GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG	TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTTACCT	GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG	AGAAG TAA
GAAAAGTTCG	GGGGCAAAAC	AAGCTCCCAG	ACGAAGAAGA	ATAGTCAGGA	ATCCTAAAGC	CTGAGCAAGT	CTTCACGAGT	GGAGTAAAGG	ATAAGCAAGA	GAGTATTACA	TACAGGAAAG	AACATCAAGA
GGAACTGGAG	CACAATTCCT	TATAAACGCC	GTTCTTCGTG	GGGGCTTGAA	CCTAGAGGCT	AACTGAAAAG	CACGAGGCCC	AGCCGCTAGA	AGACGGGCCA	GTATGACGCT	GGCCTTTGGG	GGCATGGCTT
TCGTAAGGAA	GACTCTACGC	TCGTAGATTA	ACGTGAGAGG	TAATCACTAG	AAGCAAAAGT	TTAAGGAGGT	ACGAGCAGAT	CAAAAAGGTT	TGCTGAGGGG	GGAAGCATAA	GAATATTAGA	ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA	GACACAGATG	GCCCTAGAGT	GAGGGCTTCT	GAAGGGAAGA	AAAGAAACCC	GTAAAGATAG	CTAGTTATTT	GTTGCCGTGG	GGGTACATAG	TTCGATCTCA	GCCGTTCTTA	ACTAAACAGA

Figure 17R

JDF-3 - (HMf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 63) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ACGCCCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAGATAACCGCGGAGGGCACGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAGAAGAAAAAAATTCCTCGG CAGGTCTGTGGAGGTCTTGGGTCCTTCACGCACCCGCAGGACXXXCCGGCAATCCGCGACAAATAAGGAAGCACCCCGCGGGTCATCGACATCTACGAGTACGACATACCC TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGGTTTAAACTCATGTCCTTCGAGATCGAGACGCTCTACCACGAGGGGAGAAGAGTTTGGAA ACCCTCGGGAGGGACGGGAGCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACCATAA **ACCTCCCBACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAGAG** aCgeCGGTGGCTACGTCAAGGAGCCGGAGCGGGGACTGTGGGACAATATCGTGTGTATTCTAGACTTTCGTAGTCTCTAACTCATAATCACCCACACAACGTCTCGCCAGATAC GCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATACAACGGCGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCCGTGAAGCTTT GGTCGCGCCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCC CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAATCTCCTCGATTACAGGCAACGGGCGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT CTATGCAGACACAGGCGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCCTTCTC GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAAGTACGCGGTCATCGACGAGGAGGGCCAAGATAACCACGCGCGGGGGCTTGAGATAGTCAGGCGCG ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCT **ATGCCAGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGG**TCATCAGAGAGCTTGAGGAAAAGTTCGGTTTTAAAGTCCT

FIGURE 17R (CONT.)

ACTGGAGCGAGATAGCGAAGGAGCCAGGCGAGGGTTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCCGTCAGAATTGTCAGGAAGTCACCGAAAAGCTGAGCAA GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAGGGTTTGGCCGAGAGT GITAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGGTTCGACCCGACGAGGACAAGTACGATG CGGACTACTACTACATCGAGAATCCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGC GTGGCTGAAGCCGAAGGGGAAGAAGAAG//

108 162 GCA AAG CAC GCA GGT AGA GAG CTT AGA AAG CAC AAG AGC TGA GAG GCA ATT CTT AGA GAC AAG GTA GCA GTA GAT AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA GTTGCT CCA GCA AAA AAG gcc GAG CAA GCA CCA ATT TTA AGC GAG ATC GAA GTT ATT GGA CAG AGA ATG AAA GCT ATG

Figure 17S

(HMf-like) - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 39) Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 40) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

108 GCA GAG CAC CTT GAG GAA GCA AAG CAC GCA GGT AGA CTT ATA AGA AAG GCT AAG ACC GIT AAG GIC GAA GAC AIT AAG CIC GCA AIT AAG AGC // GAA TTA CCA ATT GCC CCA GTT GAC AGA GCA AAA AAG GCA GTA GAT CTT GAG CAA GCA GCT AAG GTA CTT CAG AGA GTT AGC AAA GCT ATT GAG ATC ATG ATG GGA GCT

agcegegacteregeacaatatcetetatctagactttcetaqtctctaqcctpcaatcataatcacccacaacetctceccăgatacectcaaccecgagegetet GACATCTACGAGTACGACATACCCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGGCTTAAACTCATGTCCTTQGAQATQGA GACGCTCTACCACGAGGAGAAGAGTTTGGAACCGGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGCGTGATAACCTGGAAGAAGATCGACCTTC ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCC CTACTTCTACGCGCTCCTCAGGGACGACTCTGGCCATCGAAGAAATCAAAAAGATAACCGCGGGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGGGAGAAGGTGA AGAAAAAGTTCCTCGGCAGGTCTGTGGAGGTCTGGGGTCCTCTACTTCACGCACCCGCAGGAC**XXX**CCGGCAATCCGCGACAAATAAGGAAGCACCCCGCGGTCATC CTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAAGGACCCGGACGTGCTGATAACATACAACGGCGACAACTTC CGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACCATAAACCTCCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGC CTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCCCGGCACCGCCACCGGCAACCTCGTCGAGTGGTTCCT AGGAGCTACGACGTTGCCCCCCGAGGTCGACATTCTGCAAGGACTTCCCCGGGCTTCCATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAGGCAGAAGATAAA

GAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGATTACAGGCAACGGCGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATA CCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGGAGGAAAAAGTTCGGTTTTAAA GTCCTCTATGCAGACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACT GCCCGGCCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAAGTACGCGGTCATCGACGAGGAGGAGGCAAGATAACCACGCGCG GGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGGCGAGGCGATTTTGGAGGCGATACTCAGGCGTCGCGTGACGTTGAAGAGGCCGTCAGAATT GCACGTAGCCATAGCGAAgcGTTTGGCCGCCAGAGGTGTTAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGG CGATTCCCTTCGACGAGTTCGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGC TACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGCGTGGCTGA

Figure 17T

Pyrococcus furiosus DSM 3638, Archeael hostone (HMf-1) section 85 of 173 of the complete genome. ACCESSION No: AE010210 REGION: complement (8333..9082)
/product="pcna sliding clamp (proliferating-cell nuclear antigen)"

Nucleotide sequence (SEQ ID NO: 67)

Amino acid sequence (SEQ ID NO: 68)

18 54	36 108	54 162	72 216	90	108 324	126 378	144 432	162
DGAC	I ATA	P CCG	N AAC	I ATA	T ACA	P CCA	A GCT	×
I ATA	ი მემ	L	V GTT	L TTA	A GCA	L CTC	D GAT	Ħ
L CTT	D GAT	n AAT	g GGA	TACC	TACT	D GAC	K AAA	œ
CA O	E GAA	L	I ATT	DGAC	G GGA	V GTT	L	Ø
A GCC	TACA	D GAC	T ACA	K AAG	CAA	E	V GTC	н
F TTT	V GTT	I ATT	E GAA	A GCA	I ATT	M ATG	e gaa	ſΞij
E	K AAA	L CTG	PCCA	K AAA	T ACA	E GAG	g GGA	×
K AAA	F TTT	V GTC	E GAA	GGT	I ATA	E	L	н
A GCA	A GCG	V GTT	V GTT	R AGA	E	V GTA	V GTT	Ø
G GGT	₽ GCC	r Aga	V GTT	K AAG	L TTA	D GAT	v GTA	Ω
E GAA	E GAG	S AGT	E GAA	L	F	I ATA	V GTT	Ø
F TTT	D GAT	P CCA	Y TAT	I ATC	N AAC	L CTA	K AAG	>
v GTA	I ATA	D GAT	K AAA	X AAG	E Gaa	CCC	A GCA	'n
I ATC	L TTA	M ATG	s AGC	K AAG	E GAG	V GTT	TACT	S
E	K AAG	A GCC	F TTT	L	g GGA	R AGA	$_{ m F}$	Ø
F TTT	S AGT	R AGG	I ATA	H	K AAA	F TTT	PCCA	Д
CCA	A GCA	M ATG	s AGC	DGAC	K AAG	T ACA	L	×
M ATG	TACC	SAGC	S TCA	M ATG	L	R AGA	E GAA	>

FIGURE 17T (CONT.)

486	180 540	198 594	216 648	234	250
AAT	T ACT	A GCA	e gaa	r Aga	
GAA	r CTA	s AGC	D GAT	I ATT	
AGG	K AAG	K AAG	A GCC	Y TAC	TGA
GCC	I ATA	T ACA	K AAG	Y TAT	GAG
ATT	e Gag	E GAG	G GGA	E GAG	GAA
TTT	V GTT	E	L	M ATG	V GTT
AAA	GAA	CAA	G GGA	CAA	A AGA
ATA	Q CAG	V GTT	A AAA	M ATG	G P
AGC	TACC	e Gag	V GTT	CCC	A GCT
GAC	GAA	IATC	M ATG	M ATG	r CTG
AGT	g GGA	DGAC	D GAC	E GAA	r T.A.
GTG	E GAG	L TTG	s TCC	N AAT	F
CTA	GCA GCA	L TTA	r CTC	g GGA	ACA
TCT	K AAG	G GGA	Y TAT	F TTT	ı CIT
ပ္သင္သ	M ATG	E GAG	s AGC	K AAG	R AGA
GAT	I ATA	D GAT	V GTC	I ATA	ი გე
AAA	F TTT	E	g GGA	T ACA	E GAA
TŢ	E	I. ŽŤŢ	Y PAT	V FTT	D SAT

Figure 17U

(PCNA)-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 65) Amino acid sequence (SEQ ID NO: 68) // Amino acid sequence (SEQ ID NO: 68)

18	54	36	108	54	162
Ω	GAC	н	ATA	<u>с</u>	റ്ററ്റ
н	ATA	Ö	999	ч	CIC
'n	CTT	Д	GAT	Z	AAT
ø	CAA	ഠ	GAA		CTA
Ø	ggg	H	ACA	Ω	3AC
	TTT	>	GTT	н	ATT
闰	GAG	×	AAA	д	CTG
×	AAA	Ŀ	TTT	>	GTC CTG
ø	GCA		gcg	>	GTT
ტ	GGT	Ø	300	æ	AGA
闰	GAA	凶	GAG	ß	AGT
ſΞı	TTT	Д	GAT	Д	CCA
>	GTA	н	ATA		GAT
н	ATC	ᆸ	TTA	Σ	ATG
闰	GAA	×	AAG	æ	ပ္သင္ဟ
ſ±ι	TTT	ß	AGT		AGG
Д	CCA	Ø	GCA	Σ	ATG
Σ	ATG	H	ACC	တ	AGC

FIGURE 17U (CONT.)

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72
             90
270
                                      126
378
                         108
324
                                                   144
432
                                                                             180
540
                                                                                          198
594
                                                                                                      216
648
                                                                162
486
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702
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                         ACA
             I
ATA
                                      PCCA
                                                   A
GCT
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AAT
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ACT
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GCA
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AGA
                         gca
Gca
V
GTT
             L
TTA
                                      L
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ATT
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AGC
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GAT
            D T
GAC ACC
                         GGA ACT
                                                                A R
GCC AGG
V E P E T I G
GTT GAA CCA GAA ACA ATT GGA
                                                   V L K
GTC CTA AAA
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AAG
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GAG ATA AAG
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GCC
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GGT AAA GCA AAG
                                      V E E M E GTA GAA
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GAG
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                        G E E N F L E I T I
GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT
                                                  F T A K V V V L G E TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA
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ATA AAA
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GCT CCA AGA
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ATG
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CTA AAG AGA
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GTG AGT GAC AGC
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GTT
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                                                                                         E
                                                                            G E GGA GAA
                                                                                         D I
GAC ATC
                                                                                                                               L L CTA CTG
                                     P L I D
CCC CTA ATA GAT
V
GTT
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ATG
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ATG
                                                                                                                   GAA
S K Y E
AGC AAA TAT GAA
                                                                                                      GAC
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ACA TTC (
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CTA AAG AAG ATC
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GAG
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                                                                CIA
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                                                                            A
GCA
                                                                                          TTA
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m L}^{
m L}
                                     R V
AGA GTT (
                                                                            M K
ATG AAG
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TTT
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GCC -
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S S
TCA AGC
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ACA
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CTT GAA
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TAT GGA
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            M
ATG
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GTT
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FIGURE 17U (CONT.)

T ACC AAG P CCC စ ဗ္ဗ L AAA AAA Y K AAG CCA W TGG GAA r G s AGC T ACC CIC A GCC ₽ÇG GAC ත වූව CAG CAG V GTC r G r CTG I E GAG GAG CCC AAG GGC CGG GTC CTC DGAC ი მმც K AAG က် ကို CIC A GCC A GCC CTC s AGC ဗ္ဗဗ္ဗ s AGC A GCC **4** DGAC r CTG T ACC က ည P CCC ည် ი მვვ V GTG v GTC CTC K AAG K AAG GAC ය පු H R AGG CIT W R I CGC ATC V L GTC CTC r CTG A GCC ဗ ဗ္ဗ CTG DGAC r CTG \mathbf{F} N AAC E GAC GAG V GTC ဗ္ဗဗ္ဗ A GCC F A GCG E D GAC **₽** I V ATC GTG CAC ဗ္ဗင္ဗ K AAG k AAG Y A GCG V GTC H CAC S TCC မှ ည CIG k AAG F Y TAC Y TAC IATC E GAG I ATC k AAG E GAG GAG L D R GAC CGC A V GCG GTC A V GCG GTG G Y GAA T ACC ი მვვ L CTC Y TAC DGAC K AAG r CTG AGT GGG ATG CTG CCC CTC TTT ™ TGG R AGG 1 ი მმმ ი მცც GGC A GCC ဗ္ဗဋ္ဌ GGG R Y Y TAC CAG D GAC CTC E S TCC CTT ACC A GCG P CCG GAC V GTC K AAG L A GCC V GTG ი მვვ A GCC CA P r CTG W TGG L CTG T ACG P A CCG GCC ' A E Q L CAG CTC D GAC GAG E P CCG CGG A GCC K AAG L CTG N AAC CAC E H GCC CTC AAG E GAG ය ප GAG CAC K AAG RGC ය පු K AAG Y TAC T ACC Y CIC ය ශීශීශී F TTT ය ශ්රී L I CTC ATC STC ACT ဗ္ဗဗ္ဗ D GAC R CGG L GAC A GCG k AAG L I ATC F TTC CIC E GAG CIG DGAC s AGC A GCC န ပြင်င A GCC DGAC A GCC ဗ္ဗဗ္ဗ

FIGURE 17U (CONT.)

D 3AC A 3CC A A CIG ₽ GCC ဗ္ဗဋ္ဌ L L F R GG GG V GTG I ATC 3 3 3 3 3 ව ශීශීශී L CTG AAA CIC Y TAC E GAG T CC R AGG V GTT r CTC Y ဗ ဗ္ဗ F E GAA CTT යිදු E Y TAT CIC s AGC ဗ္ဗ R AGG CHT E GAG ACG g GC C V GTG CCG DGAT PCCT ය පි E L CTG M ATG ය පි GAG W A GCC A GCC V GTG K AAG CAC ව ල E GAG DGAC GGG A GCC s TCC CTT GAG DGAC L E D L A GAC CTG GCC LCTC GCC CCC ¥G GG GGG CGG A A A D GAC V GTG M ATG မှ ည CII CTC W M ATG CAC E GAG CTC A GCC **₽** D GAC ი ცვ g G C C R AGG s AGC မှ ည CIC ස රි CCC ဗ ဗ္ဗ E සු වූ A GCC E GAG g G G S TCC TGG. ဗ္ဗဗ္ဗ L R AGG A GCC E CAC H က ည ကို ည ස පි GAG r CTG r TTG A K GCC AAA 1 E E GAG GAG S TCC F AAG V GTC ი მვვ P CCG T ACC GAG ი მგმ V GTC gg A CTC GGC R T Y L R TAT CTC AGG E සි උදි ය වි CIC ი მმ E A GCT K AAG F L CTT L CTG s TCC ශීය A GCG g GGC N AAC A GCG CIT s TCC A GCC R AGG CTT CIG GAC R AGG CTT E GAG CTT s TCC GAG ი მვვ P K CCC AAG V A GTG GCC E D GAT V GTG K AAG ය ය CCT GAG ი მვვ P CCC V GTG R AGG GAC F TTT DGAC T ACG R AGG E CŢĞ A GCC r CTG GAA ₩ TGG g ggc M ATG F TTT s AGC A GCC GAC r CTG CIG E GAC r CTG R AGG ¥ TGG CAC д ССС ₽ GCC E GAA gcc Gcc r CTG V GTG R AGG CTG E GAG N AAC V GTG CIC L CTG F A GCC L CTG r CTG CTC A GCC Y G GGG gcc Bcc GG GG R AGG E

R AGG Y TAT IATC F A AC IATC A 3CC T ACC T ACG SAGT IATC 8 GCC CAG CAG R AGG L CTA DGAC r CTG 3 3 3 3 5 5 E r CTC M ATG ACC CTA R AGG AAC N AAC r CTG E မှ ည ი მვმ CIG ₩ TGG K AAG E GAG က် ကို ရ ၁၅ V GTC CAC L ₽ GCC GAG F ~ B SAGC A GCC CAG Gr A T GCC ACG I ATC CCC ი მმმ ₽ GCC Y ල වි V GTG GAC A GCC A GCG s TCC CAC CTA A GCC CAG CAG LCTC T ACC L TTG ဗ္ဗင္ဗ T ACC CIC යි යි × R CGC TACG S TCC E D GAC CTA E g GGC s AGC r CTG ස ට ය වි GAC ACC P A GCC V GTC ¥ TGG CTC T ACG မှ ၁၁ I ATC M ATG CAC N O T AAC CAG ACG P L က ည ი ცვ CAC CAC L CTG F s TCC K AAG CIG gg A Н Q N I CAG AAC ATC E A GCC r ශීරී E IATC မှ သွ GGC GGC CTC S TCG Œ D GAC E $_{
m L}^{
m L}$ DGAC DGAC v GTC K AAG V GTG M ATG F I ATT F V GTG CGG V GTC ဗ္ဗ IATC gcc Bcc V GTG ი მვი R AGG T Y ACC TAC ය දු CIC ი მმმ E GAG GAA T ACC မ ည I ATC R AGG A GCC Y TAC T ACC N AAC F L CTC A GCC K AAG GAG L CTG CAC EGAG 臼 s AGC ЭК CAG CAG r CCC A GCC E V GTC EGAG ₽ 300 CAG CAG සි පි K AAG CTC D GAT GGG GGG r CTC DGAC I ATA F TACG E GAG P CCC ი მვვ LCTG R CGC s TCC O CAG r CGC CGG R V GTC F K AAG ဗ္ဗ V GTC ဗ္ဗဗ္ဗ K AAG ဗ ဗ္ဗ I ATC S AGC N AAC g G G န Icc r CTC s AGC ဗ္ဗဋ္ဌ යියිය

Y V GTG ရင္ပ E A ი ი ე ცვც CAG E E ය විව r CTG TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC GGG R v GTC GCC GCC R AGG CTC M ATG R AGG ^ಹ ೧೧೧ E GAG မှ ၂ V GTC V GTC F N M TTC AAC ATG E G R GAG GGC AGG r CTG L \mathbf{F} A K E GCC AAG GAG P D CCA GAC D E GAC GAG r CTC K AAG E GAG R L V GTG V GTG A GCC CAC CIG Y TAC M ATG M ATG V GTC K T AAG ACC E R GAG CGC R R CGC CGC V A GTG GCC A GCT CAG CIG LCTT E GAG RCGC A GCC K AAG r CTC A GCC R M AGG ATG I ATT ဗ္ဗ D L M GAC CTC ATG A GCG E ₩ TGG E GCG F E R GAG AGG A GCC gg 🌣 CIC R CGG CGG TACC V GTG A GCC ი მვვ K V AAG GTG K S AAG AGC E M GAA ATG ATC CCT T A ACC GCC k AAA E GAG V GTG CCA

GAC H E H V G I G GTG GGG ATA GGG ი მვვ GGA GGC R G CGC GGC E V GTG L E 9 9 9 9 D GAT L A V P CTG GCC GTG CCC I ATT E G GAG GGC AAG ကို ည A GCC * TAA V Y GTG TAT H s TCC H LCTC

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Figure 17V

Taq DNA polymerase- (PCNA) fusion protein

Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 68) Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 67)

G G G // GGC GGC GGT

V GTG ACC AAG CCC ი მვვ L CTG Y TAC GCA P AAA V T S G M L P L F E P K G R V L L GTC ACT AGT GGG ATG CTC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG H A L K G L T CAC GCC CTC ACC CIC g CC ACG LCTG S AGC GAC ი მმც G F A K S L GGC TTC GCC AAG AGC CTC ပိုင္ပ AAG CTC A GCC E GAG GCC V D GTG GAC (**4** gcc Gcc CTG ACC မှ ည GAC CIC CAC д С V GTC V F GTC TTT A G GCG GGC (D D GAC GAC R I CGC ATC V L GTC CTC r CTG E GAG (V GTG A L I K GCC CTC ATC AAG G Y E A GGC TAC GAG GCG GGC TAC GAG GTC D R I H GAC CGC ATC CAC G G Y K A V I GCG GTG ATC TIC Q A V Y ſΞų CGC ACC ۲ ద TAC GAC s TCC Y TAC ч СП P E GAG × E K GAA AAG V GTG ත විසි CA A V GTC CTT A GCC CTG GCC 4 E D GAG GAC CCG r CTC GAG GG R E ы Д CAC GAG CIC CAG GCC CCC CAC A GCG Ħ 团 CAC 999 Y TAC AAG င္ပင္ပင္ K AAG GGC CGC $_{
m TTT}$ Ħ Ö A L GCC CTC S R AGC CGG E D GAG GAC L A CTG GCG A K GCC AAG D L GAC CTT F GAC GGC ט S TCC Ω

CAG

GAC

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G L R GGC CTG AGG

W E K Y TGG GAA AAG TAC

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T P A A A A CC CCG GCC

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A GCC A GCC A GCC X AAG GA B L DGAC CTT CIT A r G ဗ ဗ္ဗ F T ACC R AGG ဗ ဗ္ဗ ი GGG r CTG A A A V GTT CIC CIC r CTG I ATC Y E R GAG AGG (F CTT ი წმ S AGC AAG GGC B GAG GAA Y TAT s AGC CIC အင္လ PCCT D GAT မှ ည E GG R E GAG P CTG M ATG ස වි **9** V GTG CIT s TCC CGG D GAC CAC CCG A GCC E GAG D GAC က် gcc Gcc L E E W CTG GAG TGG K AAG D N GAC AAC A L GCC CTT GCC CC ದ್ದಿದ್ದ GCC CCC IATC r CTC CCC W TGG A A A D GAC v GTG ₹ 2005 CTG GAG gcc Bcc D GAC CTC TGG M ATG **4** 22 ი წვმ gcc Gcc D GAC GCC CCC R န TCC မှ ည R CGG s AGC CCC r CFC စ ညီ E L K CTG AAG K R AAA AGG A L T G D E GCC CTG ACC GGG GAC GAG W TGG က် သည် GGG R L တ္မွင္မ A GCC GAG CAC r CTT ပိုင္ပင္ပ R K AGG AAG (S R K CGC AAG F TTT GAG A G E GCG GGG GAG V GTC GCG PP ი მცი S N T T TCC AAC ACC ACC CIC ₽ 2000 CIC R CGG E GAG E CGG GG R GCG. DGAC K AAG F r CTG s TCC ရ ဝင္ပင gcg ဗ ဗ္ဗ CTT D L GAT CTG GAG E K T GAG AAG ACG r CTG GCC GAG DGAC R AGG CTT ი ცვც L CTT K N AAG AAC O E GAG (V GTG (CCT . K AAG E V GTG R AGG K AAG ဗ္ဗဗ္ဗ . රිශීල D GAC DGAC E GAG CCC F TTT CTG L CTG A GCC GAA TGG ACG A D Y GCC GAC TAC ი მმ L M ATG CTG F s AGC g GGC A GCC D GAC r Agg r CTG G I GGC ATC L R CTC AGG GAG CTC CAC P CCC GAA V GTG CIC A GCC A GCC r CTG A GCC F LCTG A GCC R AGG CTG r CTG gcc Y TAC

A N IATC A T ACC සි සි V GTG T ACG S AGT R AGG Y TAT I ATC I E A GCC LCTC Y TAC စ ညီ E 3AG CIC R AGG CTA CAG D GAC r CTG CTT F G E GAG N AAC က် ည r CTG E GAG မှ ည r CTG R AGG ი მვვ N AAC CAC A GCC A GCC F LCTT V GTC ය ලීලී ය ශීශීල CTT **₽** E GAG CTT E GAG V GTG GG PD . . A GCC Y TAC I ACG P CCG v GTG DGAC CIC CAC L A GCC CAG CTC M ATG E A GCC T ACC L TTG ဗ္ဗဗ္ဗ E ဗ္ဗဋ္ဌ LCTG R AGG CAC s AGC DGAC r CTG T ACG R CGC CTA s TCC E A GCC DGAC T ACC I ATC CCGG အ ည A GCC ₽ GCC V GTC ¥ cr Cr E K L F S TCC $_{
m LTG}$ r CTG L ITG T ACG CCC ත විවි CAC CTC R CGC R CGC CCC ව පුවු V GTC o CAG I ATC A E A GCC K AAG V GTG GAG F V GTC DGAC E GAG A GCT R AGG N AAC AAC r CTG R AGG ဝ ၁၅ I ATC I ATT s TCC CTC V GTC CAG L F A GCC V GTG L E K T AAG ACC မှ သ R AGG CIT Y TAT E Y TAC දුල් ක CTC R AGG IATC G GGG ₽ GCC Н ACC r CCC A GCC ACC N AAC F r CTC CAG A GCC E E GAG R AGG V GTG S AGC H CCC A GCC E GAG DGAC E K AAG GAG GAC CHC T ACG r CTG r CTC GAT CGG I ATA R CGG k AAG အင္လ N AAC V GTG L CTG CGC r CTG R GGC န Tcc ra CGC CAG > A GCC EGAG A GCC S TCC ဗ္ဗဗ္ဗ CIC K AAG ස් විට ဗ္ဗဋ္ဌ s AGC IATC

IATC A GCC မှ ည Y ဗ ဗ္ဗ EGAG **A** 300 a GGG V GTG ATG T ACC F ი მვვ CGG CAG r G E E GAG LCTA TGG K AAG E s AGC ය දි ₽ GCC V GTC AGG R Cic M ATG v GTC GCC AGC CAG E ကို ည မှ ည V 3TC **₽** CAG R AGG CIA M ATG F LCTG E gcg B S F TTT R AGG CGG GAC ATC CAC ACG GAG ACC റ്റു r Y TAC **့** ဗွင့် D GAC N AAC CIC E GAG K AAG ₽ GCC F TTC K AAG D GAC CGC R CCA ස ප E ය උපි r CTG M ATG CAC E E V GTG A GCC V GTG CAC r CTG V GTC R A GCC I ATT $_{
m L}$ Y TAC M ATG M ATG V A GTG GCC F CAG CCC CCC အင္လ S TCG T ACC CGC BC A GCT L LCTG D GAC k AAG E M ATG **₽** အင္လ V GTG ဗ ဗ္ဗင္ဗ CAG E GAG CGC A GCC K AAG CIC A GCC L Y CTC TAC R M AGG ATG MATG E A GCC ဗီဗ္ဗ A GCG TTC CAG GAG GGG A GCC IATT CTC ₽ GCG E GAG E TGG F E cgg _m DGAC နှင့် R AGG R CGG V GTC E GCC CIC ი ცვვ E ACC V GTG GCC မှ ပ ත විවි Y TAC ස පි GIC E M GAA ATG PCCT E GAG s AGC K AAA V GTC F V GTG gcc Gcc gg V GTG T ဗ ဗ္ဗ AAC I K AAG K AAG P CCA

W GAC EGAG ი მმმ I ATA ი გვვ G GGG ရ ရင် G GGA V GTG E ය ශීර V GTG GG PP E GAG ဗ ဗ္ဗ CTG DGAT မှ သ IATT V GTG ဗဗ္ဗ ₽ GCC E L CTG K AAG A GCC က်င္ပင္ပ S TCC H Y TAT V GTG r CTC H

18 54	36 108	54 162	72	90	108 324	126 378	144 432	162 486	180 540	198 594	216 648
D GAC	I ATA	r CCG	N AAC	I ATA	T ACA	G P	A GCT	N AAT	T ACT	A GCA	E
I ATA	ი მმმ	r	V GTT	L TTA	A GCA	L	D GAT	E GAA	L	S AGC	D GAT
L	D GAT	n AAT	G GGA	TACC	TACT	D GAC	AAA AAA	R AGG	K AAG	K AAG	A GCC
CA &	E	L CTA	I ATT	DGAC	g GGA	V GTT	L	A GCC	I ATA	T ACA	K AAG
A GCC	T ACA	D GAC	ACA	K AAG	CA &	E GAA	V GTC	I ATT	E GAG	E GAG	G GGA
F TTT	V GTT	I ATT	e Gaa	A GCA	I ATT	M ATG	E GAA	F TTT	V GTT	E GAG	L
E	K AAA	r CTG	P CCA	K AAA	T ACA	e Gag	G GGA	K AAA	E	CA O	g GGA
K AAA	F TTT	V GTC	E GAA	G GGT	I ATA	E	L	I ATA	CAG	V GTT	K AAA
A GCA	A GCG	V GTT	V GTT	r Aga	EGAG	V GTA	v GTT	S AGC	T ACC	E GAG	V GTT
G GGT	A GCC	r Aga	V GTT	K AAG	L TTA	D GAT	V GTA	D GAC	GAA	I ATC	M ATG
E	E	S AGT	E GAA	L	F	I ATA	V GTT	S AGT	G GGA	D GAC	D GAC
F TTT	D GAT	CCA	Y TAT	IATC	N AAC	L CTA	K AAG	V GTG	E	$_{ m L}$	s TCC
V GTA	I ATA	D GAT	A A A	K AAG	E GAA	CCC	A GCA	L	A GCA	L TTA	L
I ATC	L TTA	M ATG	S AGC	K AAG	E	V GTT	TACT	s TCT	K AAG	G GGA	Y TAT
E GAA	K AAG	A GCC	F TTT	L	G GGA	r Aga	F	A GCC	M ATG	E GAG	s AGC
F TTT	S AGT	r Agg	I ATA	H CAC	K AAA	F TTT	P CCA	D GAT	I ATA	D GAT	V GTC
P CCA	A GCA	M ATG	S AGC	D GAC	K AAG	T ACA	L	K AAA	F TTT	E GAA	G GGA
M ATG	TACC	S AGC	s TCA	M ATG	L	r Aga	e gaa	V GTT	E	L	Y TAT

234	702	250	
ద	AGA		
Н	ATT		
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闰	GAG	臼	GAA
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V T I K F G N E M P M Q M E Y Y I	STT ACA ATA AAG	DEGRLTFLLAPRVEE*	AAD
>	TI	Ω	TAT

Figure 17W

Pfu DNA Polymerase (WT) -(PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 67)

ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc ccccagtcgc tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag gttttatact ccaaactgag ttagtagata tgtgggggagc ataatgattt tagatgtgga ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct

cettecaatg gaaatteage ttteaagatt agttggadaa cetttatggg atgttteaag agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac aggtggatte gttaaagage cagaaaaggg gttgtgggaa aacatagtat acctagattt tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaagc aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaact tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga tagagocota tatocotoga ttataattac coacaatgtt totocogata ototaaatot gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta

atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag ctgtaaggag tgtgctgaga gcgttactgc ctgggggaaga aagtacatcg agttagtatg gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac togtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag aggogatggt ccaattagca atagggcaat tctagotgag gaataogato ccaaaaagca caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct

taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta gtagaagcgg cactactcag atgetteece aggaatgagg ttgttgtage tenteeenga tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt ttgetecaa gcagageege tecaatggat aacaeeeetg tteeegeaee caagteeget acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa

ATA CCCG AAC ATA ACA CCA GCT ACT GCA GAA AGA GGG ATA TTA GCA CTC GAT GAA CTA AGC GAT ATT CTA AAT ATT GGA ACC GAC AAA AGG AAG GCC CAA CTT ACA GAA GAT GGA ACT ದಿದ್ದ TAC TGA ACA ATT C CIA ATA ACA ggg GIT TAT AAG GAA GAC CAA GAG GGA GTC GAG TTT GTT ATT GAA GCA ATT ATG GAA TTT GTT GAG CTTATG GAG GAG AAA CTG ACA AAA AAA GAA CAA GGA CAA GGA AAA TTT GGT ATA GTC GAA GAA ATA CAG GTT AAA ATG CCA CTT GCA ggg GTT GTT GAG GTA ACC GAG GTT AGA GTT AGC GCC AGA GTT AAG ပ္ပင္ပ TTA GAT GTA GAC GAA ATG TTT GAA GGT ATC ATG CTG GAG GAC AGT CTA TTC GGA GAC GAA CTA ATA AGT GTT GAA CCA GAT ATC AAC GTG GAG AAG TTG ATA AAG GTA GAT AAA GAA TTA CIC gg GCA CTA GCA GGA TTA AAG ATG AGC GAG AAG GGA CIT GAA ATC ACT TAT GTT TCT TTTGCA AGT AAG gaa CTA $_{
m LLL}$ ATG GAG AGA AGC AAG GGA ggg TIC ATA GAT AGG ATA GIC $_{
m LLL}$ CAC AAA TTT CCA GAT ATA AGC ATG
TCA AGC
ATG GAC
CTC AAG
AGA ACA
GAA CTT
GTT AAA CCA TTTGAA GGA ACA GAA ACC GAA rat

aagattgaga tgttcttgg

Figure 17X

(PCNA) - Pfu DNA Polymerase (WT) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 61)

54	108	162	216	270	324	378	432	486	540	594	648	702	
GAC	ATA	CCG	AAC	ATA	ACA	CCA	GCT	AAT	ACT	GCA	GAA	AGA	
ATA	999	CTC	GTT	TTA	GCA	CTC	\mathtt{GAT}	GAA	CIA	AGC	GAT	ATT	
CIT	GAT	AAT	GGA	ACC	ACT	GAC	AAA	AGG	AAG	AAG	ggg	TAC	
CAA	GAA	CTA	ATT	GAC	GGA	GLL	CTA	ggg	ATA	ACA	AAG	TAT	GAG
ညည	ACA	GAC	ACA	AAG	CAA	GAA	GIC	ATT	GAG	GAG	GGA	GAG	GAA
TTT	GTT	ATT	GAA	GCA	ATT	ATG	GAA	TTT	GTT	GAG	CTT	ATG	GLT
GAG	AAA	CIG	CCA	AAA	ACA	GAG	GGA	AAA	GAA	CAA	GGA	CAA	AGA
AAA	TTT	GTC	GAA	GGT	ATA	GAA	CIT	ATA	CAG	GTT	AAA	ATG	CCA
GCA	gcg	GTT	GTT	AGA	GAG	GTA	GTT	AGC	ACC	GAG	GTT	CCC	GCT
GGT	ggg	AGA	GTT	AAG	TTA	GAT	GTA	GAC	GAA	ATC	ATG	ATG	CTG
GAA	GAG	AGT	GAA	CIA	TIC	ATA	GTT	AGT	GGA	GAC	GAC	GAA	CTA
TTT	GAT	CCA	TAT	ATC	AAC	CTA	AAG	GTG	GAG	TTG	JCC	AAT	TTC
GTA	ATA	GAT	AAA	AAG	GAA	CCC	GCA	CTA	GCA	TTA	CIC	GGA	ACA
ATC	TTA	ATG	AGC	AAG	GAG	GTT	ACT	ICI	AAG	GGA	TAT	TTT	CTT
GAA	AAG	ggg	TTT	CTA	GGA	AGA	TTC	ggg	ATG	GAG	AGC	AAG	AGA
TTT	AGT	AGG	ATA	CAC	AAA	TTT	CCA	GAT	ATA	GAT	GTC	ATA	GGA
CCA	GCA	ATG	AGC	GAC	AAG	ACA	CII	AAA	TTT	GAA	GGA	ACA	GAA
ATG	ACC	AGC	TCA	ATG	CIC	AGA	GAA	GTT	GAA	CTT	TAT	GTT	GAT

ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc ccccagtcgc tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat caactotaca cotococtat tttototott atgagatttt taagtatagt tatagagaag gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga ttacataact gaagaaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt

taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt aataccaatg gaggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt cettecaatg gaaatteage ttteaagatt agttggaeaa eetttatggg atgttteaag gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct

tagagocota tatocotoga ttataattao ocacaatgtt totocogata ototaaaatot tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaagc gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg gaaggagoto gaagaaaagt ttggatttaa agtoototao attgacactg atggtotota tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga agtaatacaa aagettgeca attatgaaat tecaceagag aagetegeaa tatatgagea gataacaaga ccattacatg agtataaggc gataggtect cacgtagetg ttgcaaagaa actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag aggogatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt

tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa gtagaagcgg cactactcag atgettecec aggaatgagg ttgttgtage tentecenga TGA aagattgaga tgttcttgg //

FIGURE 17Y

(PCNA) - PFU DNA POLYMERASE (V93 R OR E) fusion protein

// Nucleotide sequence (SEQ ID NO: 27) //Nucleotide sequence (SEQ ID NO: 28) Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 67)

AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) GAG (ALL CODONS FOR GLUTAMIC ACID) V93R MUTANT: XXX = AGA, = GAA, V93E MUTANT: XXX

216 270 378 486 540 648 162 324 432 594 702 CCG ATA ACA CCA ATA GCT AAT ACT GAA AGA GGG CHC GLI TIA GCA CIC GAT GAA CIA AGC GAT ATT TAC GAT GGA ACC GAC AAA AGG AAG AAG ggg AAT ACT CTA CTA GGA ggg ACA GAA AAG TAT ATT GAC GTT ACA GAG ACA GAC AAG GIC GAG GAG GGA CAA GAA ATT GAA TII GAA GTT ATT GCA ATG GAG GAA CTT ATG ATT TTTGTT CTG GAG CAA AGA AAA SCA AAA ACA GGA AAA GAA CAA GGA GIC GAA ATA GGT AAA GAA CIT GTT ggg GAG GTT AGC GAG ပ္ပ GTT GTT AGA GTA ACC GTT ပ္သပ္သ AAG GAC GGT AGA GTT TTA GAT GTA GAA ATC ATG GAC GAG AGT GAA CTA TIC ATA AGT GGA GAC GAA GTT GAT CTA CCA TAT AAG TCC AAC GTG GAG TTG AAT GTA ATA GAT AAA AAG GAA င္ပင္ပ GCA CTA GCA TTA CIC GGA ACA TTA AGC AAG ATG AAG TAT CIT GAG GIT TCT GGA ACT TTT ggg AGA TII AGA ggg GAG AGC AAG GGA TIC AGT AGG ATA TTT CCA GAT ATA GAT GIC ATA CAC AAA GCA ACA GAA CCA ATG AGC GAC AAG AAA LLL GAA GGA ACA CTT AGC TCA ATG CIC AGA CII TAT GAA GTT GAA GTT

540 180 300 360 420 480 AAGGCATGGA TCTTCCATAC CTGTTATTAG GCTATTCAAA CATTTACGCT AGAAAAGTT AAAGAGATAC TCTTGCCTTC GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG CAAGCCTATT TATAATGATT TAACGGGGGA CCACTATTAG TTAGACCATA TTCCATTTGC AAGGCCCAAT AGTTTCTCGG AGCTAAAGAT AAAACATAGA CATAACTGAA GAAGGAAAAC GAATACGATA GGGGAAGAAG GAGTTTGGAA GATAGAACTT GTTAAGAAAA GTTGAGAAAA CAAGATXXXC ATTACTTGGA GGAACATCCC AGCAAAGGTG GATAGAGCAT GATTGAAGAA TGTAGAGAAG GGACATCTTC ACCAATGGAG CGAAGGAGAA ATGTGGATTA GAAAATTTAA ATGATTCAAA AAGGCCTAAT ATGAAAATGA GAATTGTTGA AACTTTATT CAGCAGTTGT CCCTCTATCA TATCAAGCGA GTTGAGGTTG ATGATTTAG AGTTATGCAG AAAGAGAACG CTTCTCAGGG ACCGTGTGGA AGAGAACATC CTCATCGACA GATATAGAAA AAGATTGTGA

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1080
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 ATATTTAGCG
                                           TGTATATGAA
                                                                                                    ACTTAGGAAA
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                CGAGCCCAAG
                              TTTCGACTTG
                                                          AGCCTGGGAA
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                                                        TACGCCGACG AGATAGCAAA
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TCGCATTCCC
                             GAAGAATACA
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                                                                                                                                                              TCGCTCCTCA
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                GAGATGGAAG
                                           CACTAGAGGC
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                                                                         TACTCGATGG AAGATGCAAA
                                                                                       CAAGATTAGT
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                AAAAACTTGG GATTAAATTA ACCATTGGAA
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GGAGACTCAT
                             GAAGTCAAGG
                                                                                                                                                                                                           GCAAATTCTT
                                                                                                                                                                                                                                                     GGAGGAGAAA
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                                                                                      TCCAATGGAA ATTCAGCTTT
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                                            CCAACATACA
ACATTATAGT TACTTATAAT
                            GACGGCTGTA
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                                                                                                                                                                                                                                                                  CATAAATTCA
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                                                          GGAGAAGGTA
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                             TAGGCGATAT
                                           TAACAAGGAC
                                                                                      AAGAATTCCT
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                                                                                                                                                              TAAATCTTGA
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               AAAAGGGCAG
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AAGGATCCTG
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                                                                                      GAACTCGGGA
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                                                                                                                                                                                                                      GCAAAAGCAA
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                             ATGCAGAGAA
                                                        GCAATTTTTG
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                                                                                                                                                                                           AGACAAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                      TACGATCCCA
                                           TATCATGTAA
                                                                                                                   GCCTACGAAA
                                                                                                                                                                             AAGTTCTGCA
                                                                                                                                                                                                                                                                                 GAAGGGTTTT
                                                                                                                                                                                                                                                                                                                                                          GTAGCTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                // TGA
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Figure 17Z

PFU DNA POLYMERASE (V93 R OR E) - (PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 67)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 1020 1080 1140 1200 1260 1320 1380 1500 1440 900 840 960 TTATGGCTAT GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA CTGTTATTAG GCTATTCAAA AATACTCCTT GGGAAGAAAG TTAGACCATA CATTTACGCT CACTAGAGGC TGTATATGAA AGCCTGGGAA AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG GTGGGAAAAC CAATGTTTCT AAAGAAAAAG GCTTGAATAT TAACGGGGGA AAGGCATGGA TTCCATTTGC AAAGAGATAC TATAATGATT GGAGACTCAT TCGCATTCCC ATATTTAGCG GGCAACTTAT TGGACAACCT ACTTAGGAAA AGTAGGCCAC GTTAGAGGAA CCTCTACATT CAAGCCTATT AGAAAAGTT TCTTGCCTTC TCTTCCATAC TATCAGGGAG CGAGCCCAAG TTTCGACTTG Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 67) GLUTAMIC ACID) CCACTATTAG AAAACATAGA TTCTCAGGAT TACGCCGACG AGATAGCAAA CTATAGAAAA AGTTTCTCGG GGGGAAGAAG AGCTAAAGAT GAGTTTGGAA AAGGCCCAAT GAGATGGAAG GAAGAATACA AGTIGCCAAA TACTCGAIGG AAGAIGCAAA CAAGATTAGT AACCTIGIAG AGIGGIICII TGGATTCGTT AAAGAGCCAG AAAAGGGGTT CCCTCGATTA TAATTACCCA TCGCTCCTCA TGGGACATTT TCTACGGATA TTACTGCCTG GAAAAGTTTG GATTTAAAGT GTGAGGAAAT GACTGCTAGA V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT GTTAAGAAAA GTTGAGAAAA CAAGATXXXC GAATACGATA ATTACTTGGA GAGAGATG ATAAAGAGAT ACCATTGGAA GAAGTCAAGG CCAACATACA ATTCAGCTTT AACTATGATA CCAAGTCTCT ACTCAAGATC GCAAATTCTT GCTGAGAGCG CATAAATTCA AAGCTCCCTG GGAGGAGAAA V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, TGTAGAGAAG GATTAAATTA TCCAATGGAA GATTGAAGAA GGAACATCCC GGACATCTTC ACCAATGGAG GACGGCTGTA GGAGAAGGTA AAGCACAGGG GGGATGCAAG TGGTTTTATA AATGAAGGAA CGAAGGAGAA AGCAAAGGTG TACTTATAAT AATAAATCTC AGCCCTATAT AAAACTCTTA TAAGGAGTGT GGAGCTCGAA AACTATCCCA ATGATTCAAA AAGGCCTAAT TAACAAGGAC ACCTTGAGAG GAAACGAAGT TAGATTTTAG GAATTGTTGA AACTTTATTT CAGCAGTTGT ATGAAAATGA AAAAACTTGG GAAAGCCAAA AAGAATTCCT TTTCAAGGTC GCTACACAGG TAAATCTTGA TTAAGACAAA AAAAAGCGAT GATGGTACTG TAGTATGGAA TTGTAAAATA CCCTCTATCA TATCAAGCGA ACATTATAGT TAGGCGATAT AGGACATCCC GICICIAIGC GACTATAGAC CTTCTCAGGG AGTGGAGAGA GCTCTAGAAT AAGATTGTGA ACCGTGTGGA CTCATCGACA GATATAGAAA AGTTATGCAG AAAAGGGCAG TATCATGTAA GAACTCGGGA GCCTACGAAA AGACAAAAGA AGAGAACATC GTTGAGGTTG AAGGATCCTG GCAATTTTG CTCAGGGAGA ATAGTATACC CCCGATACTC GCAAAAGCAA ATGCAGAGAA TTATGGGATG AAGTTCTGCA TACATCGAGT GACACTGATG

1980 2040 2100 2160 2220 2280 2328 TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA TGAAGAAGCT TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT AGCTGAGGAA GGTTCTTCCA TITGGAGACA ATACTAAAAC ACGGAGATGT GGGCAATTCT TGGAGAACCA ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // CGATGGTCCA ATTAGCAATA GAATATTACA GTATGACGCA ATGAGCAGAT AAGCTAGAGT CAAAGAAACT TACTTAGAGG AAAAGCACAA GGATATTGGA CTCGCAATAT GTGAGAATAG TACGATCCCA GTAGCTGTTG GGATACATAG GCGGTACTTA GAAGGAAAAG AAAGAAACTC

324 378 540 162 216 270 432 486 594 648 702 ATA GCT ACT CCG ACA CCA GCA GAA GTT TTA GAA CTC GCA CIC GAT CTA AGC GAT ATT GAT AAT GAC TAC GGA ACT AAA AGG AAG ပ္သင္ဟ ACC AAG CTA CTA ATA GCC GGA ACA GAC GLI ACA ATT GGA AAG GAG TAT AAG GAG ACA GAC CAA ATT GAG GAA GTC GTT ATT GAA GCA ATT ATG GAA TTT GLT GAG CTT CTG GAG CCA ACA GGA CAA AAA GGA AAA GAA GA ATA ATA GAA GGT GAA CHI CAG GLT GCA GTTGLL GAG AGC GIT CCC AGA GTA GIT ACC GAG gg GAC ATG AGA AAG TTA GAA ATC GIT GAT GTA ATG CTA GAC GAC AGT GAA AGT GAA TIC ATA GTT GGA CCA CTA GTG GAT TAT ATC TTG AAC AAG GAG GAT AAA AAG CIC GGA ATA GAA ပ္ပပ္ပ GCA CTA TTA GCA ATC TTA ATG AGC AAG GAG GTT TCT AAG GGA TAT ACT LLI ggg TTTTIC ATG GAG AGC AAG GGA ggg AGA ATA GTC GAT AGT AGG CAC AAA TTT CCA GAT ATA GCA ATG AGC AAA CCA AAG ACA GGA ACA GAC CHH TTT GAA GAA AGC TCA AGA GAA GTT TAT GTT ACC GAA CTT ATG

Figure 17AA

PPU DNA POLYMERASE (G387P/V93R OR E) - (PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 67)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 1260 1500 1620 1680 1020 1080 1140 1200 1320 1380 1440 1560 1740 009 540 840 999 900 or T) AATAGATGAA AAGGCATGGA AGAAAAAGTT GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA ACTTAGGAAA TCAAAGAAGG AATACTCCTT TTATGGCTAT GCTTGAATAT TGAAGAAGCT TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG CTGTTATTAG GCTATTCAAA CATTTACGCT CAAGCCTATT AAAGAGATAC TCTTGCCTTC TATAATGATT TCTTCCATAC TATCAGGGAG ATATTAGCG CGAGCCCAAG TTTCGACTTG TGTATATGAA GGCAACTTAT TGGACAACCT GTGGGAAAAC CAATGTTTCT AGTAGGCCAC GTTAGAGGAA GGGAAGAAAG CCTCTACATT AAAGAAAAAG TGAAATTGCA G387P Mutant (CCN is the codon for Proline where N = C, G, A, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) TTAGACCATA TAACGGGGGA CCACTATTAG TTCCATTTGC GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TCGCATTCCC CACTAGAGGC AAGCACAGGG AACCTTGTAG AGTGGTTCTT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA CTATAGAAAA GTGAGGAAAT GGTATGCAGT AGTTTCTCGG GGGGAAGAAG AGCTAAAGAT AAGGCCCAAT GAGATGGAAG GAAGAATACA AGTIGCCAAA TACTCGAIGG AAGAIGCAAA TCCAATGGAA ATTCAGCTTT CAAGATTAGT TAATTACCCA TCGCTCCTCA TGGTTTTATA CCAAGTCTCT TGGGACATTT TCTACGGATA TTACTGCCTG AAAACATAGA AAAGAGCCAG AAAAGGGGTT GATTTAAAGT GACTGCTAGA GAGATTGGAG ACGGAGATGT ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CAAGATXXXC GAATACGATA GAGTTTGGAA TACTTATAAT GGAGACTCAT GTTAAGAAAA GTTGAGAAAA ATTACTTGGA GACGGCTGTA GAAGTCAAGG CCCTCGATTA AACTATGATA GATAGAACTT ACCATTGGAA AATGAAGGAA ACTCAAGATC GCTGAGAGCG GGAGGAGAAA CATAAATICA AAGCICCCIG ATTCTTCGTT ACGAAGAAGA TGGTTTAGAG ATAGTTAGGA V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CCAACATACA AAAACTCTTA GCAAATTCTT GAAAAGTTTG TTTGGAGACA ATACTAAAAC GAAAATTTAA GATAGAGCAT GGAACATCCC CGAAGGAGAA NGGATTCGTT GGGATGCAAG GATTGAAGAA TGTAGAGAAG GATTAAATTA AGCCCTATAT GGACATCTTC ACCAATGGAG AGCAAAGGTG AATAAATCTC AACTATCCCA TAAGGAGTGT GGAGCTCGAA ATGATTCAAA TTTCAAGGTC AACTTTATT GAAAGCCAAA ACCTTGAGAG GAAACGAAGT AGGACATCCC TTAAGACAAA AAAAAGCGAT GTCTCTAIGC GAATTGTTGA CAGCAGTIGI AAGGCCTAAT ACATTATAGT TAACAAGGAC GCTACACACC TAGATTTTAG ATAAGAGGG ATGAAAATGA TATCAAGCGA AAAAACTTGG TAGGCGATAT AAGAATTCCT GATGGTACTG CCCTCTATCA TAAATCTTGA TAGTATGGAA TTGTAAAATA TCATTACTCG AAGCTAGAGT CTTCTCAGGG AAAGAGAACG ACCGTGTGGA AGTTATGCAG AAGGATCCTG AGTGGAGAGA GCCTACGAAA CCCGATACTC AAGTTCTGCA AGACAAAAGA TACATCGAGT GTGAGAATAG AAGATTGTGA CTCATCGACA GATATAGAAA GTTGAGGTTG AAAAGGGCAG ATGCAGAGAA TATCATGTAA TTATGGGATG CTCAGGGAGA ATAGTATACC GACTATAGAC GCAAAAGCAA GACACTGATG GAAGGAAAAG AAAGAAACTC AGAGAACATC GCAATTTTG GAACTCGGGA GCTCTAGAAT GAAGGGTTTT

2100 2160 2220 2280 2328 TTACATGAGT ATAAGGCGAT AGGTCCTCAC TAAAGCCAGG AATGGTAATT TACAGAAAGG AAGACCTCAG ATACCAAAAG AGCTGAGGAA GGTTCTTCCA GGGCAATTCT TGGAGAACCA TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // GGAGTTAAAA ATTAGCAATA GAATATTACA CGATGGTCCA CAAAGAAACT AGCTGCTAAA GGGATTTGGA CTCGCAATAT ATGAGCAGAT AACAAGACCA GTATGACGCA GGATATTGGA TACTTAGAGG AAAAGCACAA GTAGCTGTTG GGATACATAG TACGATCCCA GCGGTACTTA ACAAGACAAG

162 216 270 324 378 432 486 540 594 648 CCG ATA ACA CCA GCT AAT ACT GCA AGA GTT AAC CIC TTA GCA GAT GAA CIA ATT CIC AGC GAT TAC ggg GAT GGA ACC ACT GAC AAA AAG AAG CTA AAT AGG GAA CTA ggg ATA TAT GAC GTT ACA AAG GGA ATT GAC ACA GAG ACA GGA GAG GAG GAA CAA GTCAAG GAA ATT GTT ATT GAA TTTGCA GAG ATT ATG GAA TTT GTT CTT ATG CIG AGA AAA CCA AAA ACA GAG GGA AAA GAA GGA CAA CAA TTTATA GIC GGT ATA CIT CAG GTT AAA GAA GAA ATG gag GAG GTT GTT GTT AGA GTA GTT AGC ACC GAG GGT AGA AAG GAT GTT TTA GTA GAC GAA ATC ATG ATG AGT GAC GAC GAA GAA GAG GAA CTA TIC ATA GTTAGT GGA CCA CIA ATA GAT AAG TAT AAC GTG GAG TIG AAT TCC GTA GAT AAG GAA GCA CCC CTA GCA TTA ATC TTA ATG AGC AAG GAG TCT GGA CTT GIT ACT AAG TAT TTT GAA AAG ggg AAG TTT CTA GGA AGA TIC ggg ATG GAG AGC AGA AGT GGA ATA TII GIC CCA ATG AGG CAC AAA ATA GAT GAT GCA AAG AGC ACA GGA ACA GAC CLI AAA TTI GAA AGC TCA CIC AGA GAA CTTATG GIT GAT ACC GTT GAA TAT

Figure 17BB

(PCNA) - PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 30) Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 29)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) or I) G387P Mutant (CCN is the codon for Proline where N = C, G, A, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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270
                         378
                                   486
                                         540
                                              594
                                                    648
     162
          216
                    324
                              432
                                                         702
               ATA
                         SGA
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          AAC
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                                         GCA
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           AAA
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                         CCC
                               GCA
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                                               TTA
          AGC
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                                         AAG
                                              GGA
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                         ACA
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1020 1080 1140 1200 909 999 720 780 840 006 960 540 GAGTITGGAA AAGGCCCAAT TATAATGATT ATATTTAGCG ACTTAGGAAA CAATGITICI CCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC CIGITATIAG GCIATICAAA CATTTACGCT AAGGCATGGA CAAGCCTATT AGAAAAGTT AAAGAGATAC GGGGAAGAG AGCTAAAGAT TCTTGCCTTC AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC TATCAGGGAG CGAGCCCAAG TTTCGACTTG TGTATATGAA AGCCTGGGAA GGCAACTTAT TGGACAACCT TCAAAGAAGG GTGGGAAAAC CCACTATTAG TTAGACCATA GTTAAGAAA TAACGGGGA TTCTCAGGAT CACTAGAGGC AGATAGCAAA CAAGATTAGT AAGCACAGGG AACCTTGTAG AGTGGTTCTT AAGCCAAGTG AAGAGGAGTA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG TTCCATTTGC TCGCATTCCC GAGATGGAAG GAAGAATACA AAAGAGCCAG AAAAGGGGTT TAATTACCCA AAGATGCAAA GAATACGATA GGAGACTCAT AGCCCTATAT CCCTCGATTA ATGTGGATTA CATAACTGAA GAAGGAAAAC GATAGAGCAT GATAGAACTT CAAGATXXXC GAGAGATG ATAAAGAGAT GATTAAATTA ACCATTGGAA GACGGCTGTA GAAGTCAAGG CCAACATACA TACGCCGACG TACTCGATGG TCCAATGGAA ATTCAGCTTT ACCAATGGAG AGCTCCAAAC NGGATTCGTT GGAACATCCC CGAAGGAGAA TACTTATAAT GGAGAAGGTA AGTTGCCAAA GATTGAAGAA GGACATCTTC AATAAATCTC ATGAAAATGA GAATTGTTGA GAAAATTTAA ATGATTCAAA AACTTTATTT CAGCAGTTGT AAGGCCTAAT CCCTCTATCA TATCAAGCGA ACATTATAGT AAAAACTTGG TAGGCGATAT TAACAAGGAC GAAAGCCAAA ACCTTGAGAG AAGAATTCCT TTTCAAGGTC GAAACGAAGT GCTACACACC TAGATTTTAG GAACTCGGGA CTCATCGACA AGTTATGCAG GTTGAGGTTG AAGGATCCTG ATGCAGAGAA TATCATGTAA GCAATTTTG TTATGGGATG GCCTACGAAA ATAGTATACC ATGATTTAG AAAGAGAACG CTTCTCAGGG AAGATTGTGA ACCGTGTGGA GATATAGAAA AAAAGGGCAG AGTGGAGAGA CTCAGGGAGA AGAGAACATC

1620 1740 1800 1860 TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920 2040 2100 2160 GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280 AAAGAAAAG 1680 CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980 1440 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT GGGAAGAAAG CCTCTACATT GCTTGAATAT TGAAATTGCA AGGTCCTCAC AGCTGAGGAA TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA AATAGATGAA AATGGTAATT ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //TAG GGGCAATTCT AACTATCCCA GGAGGAGAAA GTGAGGAAAT TTACATGAGT ATAAGGCGAT TAAAGCCAGG TCTACGGATA CATAAATICA AAGCICCCIG GACIGCIAGA TTACTGCCTG GGAGCTCGAA GAAAAGTTTG GATTTAAAGT GGTATGCAGT GAGATTGGAG TAAGGAGTGT GCTGAGAGCG TGGTTTAGAG ATAGTTAGGA AGCTGCTAAA GGAGTTAAAA CGATGGTCCA ATTAGCAATA AAAACTCTTA GCAAATTCTT ACGAAGAAGA AACAAGACCA ATTCTTCGTT AATACAAAAG AGGACATCCC AAGCTAGAGT AAAAAGCGAT TAAAAGAAGT ATGAGCAGAT AAAAGCACAA GGATATTGGA GATGGTACTG TAGTATGGAA GTCTCTATGC TTGTAAAATA ATAAGAGGGG TCATTACTCG CAAAGAAACT TACTTAGAGG TACGATCCCA AAAGAAACTC AAGTTCTGCA GACTATAGAC TACATCGAGT GTGAGAATAG GGATACATAG GCGGTACTTA GAAGGAAAAG CTCGCAATAT GTAGCTGTTG SCAAAAGCAA GACACTGATG GCTCTAGAAT GAAGGGTTTT

Figure 17CC

(PCNA) - PFU DNA POLYMERASE (D141A/E143A/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 31) Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 32)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

108 162 216 CTC CCG GTT AAC GGG ATA CII GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA ACA GAA GAT TIT GCC CAA GTA TIT GAA GGT GCA AAA GAG TIT ATA GAT GAG GCC GCG TIT AAA GIT TTA GAA ATC AGC ATG AGG GCC ATG ATG CCA TTT GAA ACC GCA AGT AAG

270	324	378	432	486	540	594	648	702		
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GCTACACA GIT GGAITCGIT AAAGAGCCAG AAAAGGGGTI GIGGGAAAAC 1200 GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 TAGATITITAG AGCCCTATAT CCCTCGAITA TAATIACCCA CAATGITICI 1260 TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 1440 AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TITCAAGGIC AAGCACAGGG AACCITGIAG AGIGGITCIT ACTIAGGAAA 1080 900 960 999 840 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 //AIGAITING AIGIGGAITA CATAACIGAA GAAGGAAAAC CIGITAITAG GCIATICAAA AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG TGTATATGAA GGCAACTTAT AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAG TAACGGGGGA AAGGCATGGA GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG TACGCCGACG AGATAGCAAA AGCCTGGGAA AATACTCCTT TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT AAAGAGATAC AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG CAAGCCTATT AGAAAAAGTT TATAATGATT TCTTCCATAC TTCTCAGGAT TATCAGGGAG CCAACATACA CACTAGAGGC GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CCACTATTAG GGACATCTTC GAATACGATA TTCCATTTGC CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT AGCAAAGGTG ATTACTTGGA AAAACATAGA AGTIGCCAAA TACTCGAIGG AAGAIGCAAA CTATAGAAAA GAGAGATG ATAAAGAGAT GATTGAAGAA GTTAAGAAAA CAAGATXXXC TTAAGACAAA AATGAAGGAA ACTCAAGATC GGAGAAGGTA GGAACATCCC TAACAAGGAC AATAAATCTC ACCTTGAGAG ATGAAAATGA AAAAACTTGG ATGATTCAAA AACTTTATTT CAGCAGTTGT CCCTCTATCA TATCAAGCGA ACATTATAGT TAGGCGATAT GAAAGCCAAA AGTTATGCAG GAACTCGGGA GCCTACGAAA CCCGATACTC GACTATAGAC CTTCTCAGGG CTCATCGACA GCNATAGCNA GTTGAGGTTG AAAAGGGCAG ATGCAGAGAA TATCATGTAA GCAATTTTG AGTGGAGAGA TTATGGGATG CTCAGGGAGA ATAGTATACC AAGTTCTGCA GCAAAAGCAA AAGATTGTGA ACCGTGTGGA AGAGAACATC AAGGATCCTG AGACAAAAGA

1860 1920 1980 2040 2100 2160 2280 2220 AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG GCTTGAATAT GAGATTGGAG TGAAATTGCA AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT AATAGATGAA AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT GGTTCTTCCA AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAG AGGTCCTCAC AGCTGAGGAA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG CATAAATTCA AAGCTCCCTG GACTGCTAGA ATTCTTCGTT ACGAAGAAGA GGTATGCAGT ATAAGGCGAT GTATGACGCA GAATATTACA TGGAGAACCA GGGCAATTCT ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // TGGTTTAGAG ATAGTTAGGA TTACATGAGT CGATGGTCCA ATTAGCAATA AACAAGACCA TAAAAGAAGT GTCTCTATGC GAAGGAAAAG TCATTACTCG CAAAGAAACT TTGTAAAATA ATAAGAGGGG ATGAGCAGAT TACTTAGAGG TACGATCCCA AAAAGCACAA GGATATTGGA GTGAGAATAG CTCGCAATAT GTAGCTGTTG SACACTGATG GCTCTAGAAT GAAGGGTTTT GGATACATAG GCGGTACTTA

Figure 17DD

- (PCNA) fusion protein PFU DNA POLYMERASE (D141A/E143A/V93R OR E)

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) G, A, or T) D141A/E143A Mutant (GCN is the codon for alanine where N = C, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA CATTTACGCT GTTAAGAAAA TAACGGGGGA AAGGCATGGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT AGAAAAAGTT GGACATCTIC GAATACGATA TICCATTIGC AAAGAGATAC CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT TTAGACCATA CCACTATTAG ACCAATGGAG GGGGAAGAAG AGCTAAAGAT GATAGAGCAT GATAGAACTT GGAACATCCC CAAGATXXXC GATTGAAGAA GAAAATTTAA ATGATTCAAA GAATTGTTGA AAGGCCTAAT CCCTCTATCA AACTTTATTT CAGCAGTTGT CTTCTCAGGG ACCGTGTGGA CTCATCGACA GCNATAGCNA AAAGAGAACG AAGATTGTGA AGAGAACATC

AGTTATGCAG	ATGAAAATGA	AGCAAAGGTG	ATTACTTGGA	AAAACATAGA	TCTTCCATAC	540
GTTGAGGTTG	TATCAAGCGA	GAGAGAGATG	ATAAAGAGAT	TTCTCAGGAT	TATCAGGGAG	009
AAGGATCCTG	ACATTATAGT	TACTTATAAT	GGAGACTCAT	TCGCATTCCC	ATATTTAGCG	099
AAAAGGGCAG	AAAAACTTGG	GATTAAATTA	ACCATTGGAA	GAGATGGAAG	CGAGCCCAAG	720
ATGCAGAGAA	TAGGCGATAT	GACGGCTGTA	GAAGTCAAGG	GAAGAATACA	TTTCGACTTG	
TATCATGTAA	TAACAAGGAC	AATAAATCTC	CCAACATACA	CACTAGAGGC	TGTATATGAA	840
GCAATTTTTG	GAAAGCCAAA	GGAGAAGGTA	TACGCCGACG	AGATAGCAAA	AGCCTGGGAA	006
AGTGGAGAGA	ACCTTGAGAG	AGTTGCCAAA	TACTCGATGG	AAGATGCAAA	GGCAACTTAT	960
GAACTCGGGA	AAGAATTCCT	TCCAATGGAA	ATTCAGCTTT	CAAGATTAGT	TGGACAACCT	1020
TTATGGGATG	TTTCAAGGTC	AAGCACAGGG	AACCTTGTAG	AGTGGTTCTT	ACTTAGGAAA	1080
GCCTACGAAA	GAAACGAAGT	AGCTCCAAAC	AAGCCAAGTG	AAGAGGAGTA	TCAAAGAAGG	1140
CTCAGGGAGA	GCTACACA G1	GTT_GGATTCGTT	AAAGAGCCAG	HAAAGGGGTT	. GTGGGAAAAC	1200
ATAGTATACC	TAGATTTTAG	AGCCCTATAT	CCCTCGATTA	TAATTACCCA	CAATGTTTCT	1260
CCCGATACTC	TAAATCTTGA	GGGATGCAAG	AACTATGATA	TCGCTCCTCA	AGTAGGCCAC	1320
AAGTTCTGCA	AGGACATCCC	TGGTTTTATA	CCAAGTCTCT	TGGGACATTT	GTTAGAGGAA	1380
AGACAAAAGA	TTAAGACAAA	AATGAAGGAA	ACTCAAGATC	CTATAGAAAA	AATACTCCTT	1440
GACTATAGAC	AAAAAGCGAT	AAAACTCTTA	GCAAATTCTT	TCTACGGATA	TTATGGCTAT	1500
GCAAAAGCAA	GATGGTACTG	TAAGGAGTGT	GCTGAGAGCG	TTACTGCCTG	GGGAAGAAAG	1560
TACATCGAGT	TAGTATGGAA	GGAGCTCGAA	GAAAAGTTTG	GATTTAAAGT	CCTCTACATT	1620
GACACTGATG	GTCTCTATGC	AACTATCCCA	GGAGGAGAAA	GTGAGGAAAT	AAAGAAAAG	1680
GCTCTAGAAT	TTGTAAAATA	CATAAATTCA	AAGCTCCCTG	GACTGCTAGA	GCTTGAATAT	1740
GAAGGGTTTT	ATAAGAGGG	ATTCTTCGTT	ACGAAGAAGA	GGTATGCAGT	AATAGATGAA	1800
GAAGGAAAAG	TCATTACTCG	TGGTTTAGAG	ATAGTTAGGA	GAGATTGGAG	TGAAATTGCA	1860
AAAGAAACTC	AAGCTAGAGT	TTTGGAGACA	ATACTAAAAC	ACGGAGATGT	TGAAGAAGCT	1920
GTGAGAATAG	TAAAAGAAGT	AATACAAAAG	CTTGCCAATT	ATGAAATTCC	ACCAGAGAAG	1980
CTCGCAATAT	ATGAGCAGAT	AACAAGACCA	TTACATGAGT	ATAAGGCGAT	AGGTCCTCAC	2040
GTAGCTGTTG	CAAAGAAACT	AGCTGCTAAA	GGAGTTAAAA	TAAAGCCAGG	AATGGTAATT	2100
GGATACATAG	TACTTAGAGG	CGATGGTCCA	ATTAGCAATA	GGGCAATTCT	AGCTGAGGAA	2160
TACGATCCCA	AAAAGCACAA	GTATGACGCA	GAATATTACA	TGGAGAACCA	GGTTCTTCCA	2220
GCGGTACTTA	GGATATTGGA	GGGATTTGGA	TACAGAAAGG	AAGACCTCAG	ATACCAAAAG	2280
ACAAGACAAG	TCGGCCTAAC	TICCIGGCII	AACATTAAAA	AATCC //		2328

54	108	162	216	270	324
GAC	ATA	CCG	AAC	ATA	ACA
ATA	999	CIC	GTT	TTA	GCA
CIL	GAT	AAT	GGA	ACC	ACT
CAA	GAA	CTA	ATT	GAC	GGA
ggg	ACA	GAC	ACA	AAG	CAA
			GAA		
			CCA		
AAA	TTT	GIC	GAA	GGT	ATA
			GTT		
GGT	GCC	AGA	GTT	AAG	TTA
GAA	GAG	AGT	GAA	CIA	TIC
TII	GAT	CCA	TAT	ATC	AAC
GTA	ATA	GAT	AAA	AAG	GAA
ATC	TTA	ATG	AGC	AAG	GAG
GAA	AAG	ggg	$_{ m TTT}$	CTA	GGA
TTT	AGT	AGG	ATA	CAC	AAA
CCA	GCA	ATG	AGC	GAC	AAG
		AGC		ATG	

378	432	486	540	594	648	702	
CCA	GCT	AAT	ACT	GCA	GAA	AGA	
CIC	GAT	GAA	CIA	AGC	GAT	ATT	
GAC	AAA	AGG	AAG	AAG	ပ္ပင္ပ	TAC	TGA
GTT	CTA	ggg	ATA	ACA	AAG	TAT	GAG
GAA						GAG	GAA
ATG						ATG	
GAG	GGA	AAA	GAA	CAA	GGA	CAA	AGA
GAA	CTT	ATA	CAG	GTT	AAA	ATG	CCA
GTA	GIT	AGC	ACC	GAG	GTT	CCC	GCT
GAT	GTA	GAC	GAA	ATC	ATG	ATG	CTG
ATA	GTT	AGT	GGA	GAC	GAC	GAA	CTA
CTA	AAG	GTG	GAG	TTG	TCC	AAT	TTC
CCC	GCA	CTA	GCA	TTA	CIC	GGA	ACA
GTT	ACT	TCT	AAG	GGA	TAT	TTT	CII
AGA	TTC	ပ္ပင္ပ	ATG	GAG	AGC	AAG	AGA
TTT	CCA	GAT	ATA	GAT	GTC	ATA	GGA
ACA	CIT	AAA	TTT	GAA	GGA	ACA	GAA
AGA	GAA	GTT	GAA	CTT	TAT	GTT	GAT

Figure 17EE

ROD DNA POLYMERASE - (PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) 540 900 99 840 CTGTCATAAG AATTTTCAAG CTTCTACGCC GAGACCAGTT GGACAAGATA CAAGCGCTAC GCTCGCCTTC TCTCCCCTAC TGTGAAGGAG CTATCTGAAA CGAGCCGAAG AGCCTGGGAA ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC GAGGCACGGG CCTTATGATA CTTCGATCTC CGTTTATGAA GLUTAMIC ACID) TTGAACCCTA TACGCTGAGG AAATAACCAC TAACCGCCGA AGTTCCTCGG CAGCGATAAG TACCCTTCGC GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TCGACTTCGC GACGGATACA CGCTTGAGGC GGCGACGAGG AGCTGAAAAT AGGGGCCAAT AGAACGTGGA GGGATGGAAG V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT GTCAAGAAGA GTTCAGAAGA CAGGACXXXC GAGTACGACA GAGTTCGCCG ATAACTIGGA GGCGACAACT GCCCTCGGAA GAAGTGAAGG CCCACATACA GGCCAGGGTG CATTGAGGAA GGTTGAAAG AACTCTACTT TACTCATCCG CAGCAGTTAT TGACATCTAC GCCAATGGAA AACCTACAAC GGAGAAGGTT TGAGGGCGAG AATAAACTTC GTTTGCCGTC GATAAACCTG CGGTTAAGCG AAAAGCTCGG TGGGCGACAG GTCAGCCGAA ACGATTCTGC AGGGATTAGT ACGAGGAAGG TCTCGACGGA ACGITCICAL TAAGACGGAC CTCTCTACCA CTCCTGAAGG GAGGTCTGGA CTCATAGACA AAAGACCCGG GCCGTCTTCG CGAGAGCATC AGCTACGCCG GTTGACGTCG TATCCTGTGA ACGGTTGTAA GACATTGAAA AAGCGCTGTG ATTCAGAGGA

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1620
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                         GGCCAGAAGA
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                                                   CGICICGCCG
                                                              CGGCCACCGC
                                                                            AGAGGAGAGG
                                                                                                      CGGCTATGCA
                                                                                                                  AAGGGAGTAC
                                                                                                                               CTACAGCGAC
                                                                                                                                                           CGAGTACGAG
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CGGCCAGTCC
            CCTCAGGAAG
                                                                                          GCTCCTCGAT
                                                                                                                                             AAAGAAGGCT
                                                                                                                                                                                                                            TCCCCACGTT
                                                                                                                                                                                                                                                      CGACGAGITC
                                                                                                                   CGGCCTGGGG
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                                    GAGGGTTGTG
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CTCGCTTAAT
                        AAAAGGAGCT
                                                   TCACCCACAA
                                                              CCCCACAGGT
                                                                            GAGACCTCCT
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            AGTGGTTCCT
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GCCCAGCTTT
            CAGCACTGGC AACCTCGTTG
                        AAGCCCGATG
                                      GAGCCCGAGA
                                                 TCAATCATCA
                                                              TATGACGTTG
                                                                            AGCCTGCTTG
                                                                                         ATTGACCCGA
                                                                                                      AACAGCTACT
                                                                                                                    GAGAGCGTAA
                                                                                                                               GATAGAGGAA AAGTACGGCT
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                                                                                                                                                          CTTCCGGGCG
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                                                                                                                                                                                                                                        GTCAAAATAC
                                                                                                                                                                                                                                                      GGCGACAGGG
                                                              ATGCAAGGAA
                                                                                        GAAGGCCACG
                                                                                                                  GGAGTGTGCA
TCCGATGGAG
                        GGCCCCGAAC
                                                 CCTGTACCCC
                                                                            ATTTATCCCG
                                                                                                                                             AATACCTGGA
                                                                                                                                                                       CTTCGTCACG
                                                                                                                                                                                    ACTIGAGALT
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                                                                                                      GATCCTGGCA
                                                                                                                                                           CAACGCCAAA
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                                                                                                                                                                                                                                                                   CGACGCCGAG
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                                      CTATGTAAAA
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                                                              ACAGAGAAGG
                                                                            ACTTCCCAGG
                                                                                                                   GGTACTGCAA
                                                                                                                               CCATCAAGGA
                                                                                                                                             TTTTGCCAC
                                                                                                                                                           TCAAGTATAT
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                                                                                                                                                                                    CAACGCGCGG
                                                                                                                                                                                                                                        AGAGGTTGGC
                                                                                                                                                                                                                                                      TCAAGGGCTC
AGGAGTTCCT
            TCTCCCGCTC
                        GGAATGAGCT
                                      ATGAAGGAGG
                                                   ATTTAGATC
                                                                                          AGAAGAAGAT
                                                                                                      GGGCCATCAA
                                                                                                                                                                                                 CGAGGGTTCT
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SAGCTTGGGA
                                                   GTGTACCTAG
                                                                GATACGCTCA
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            CTCTGGGACG
                        GCCTATGAGA
                                    CGGCAGAGCT
                                                                                                      TACAGGCAGA
                                                                                                                   AGGCCCCCT
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                                                                                                                                             ACCGACGGAT
                                                                                                                                                           ATGGAGTTCC
                                                                                                                                                                                                                            GTGATCCACG
                                                                                                                                                                                                                                                      TACATCGTGC
                                                                                                                                                                                                                                                                   GACCCGACGA
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u)	10	16	21	27	32	37	43	48	54	53	64	7	
GAC	ATA	CCG	AAC	ATA	ACA	CCA	GCT	AAT	ACT	GCA	GAA	AGA	
ATA	GGG	CIC	GLT	TTA	GCA	CIC	GAT	GAA	CTA	AGC	GAT	ATT	
CHI	GAT	AAT	GGA	ACC	ACT	GAC	AAA	AGG	AAG	AAG	ggg	TAC	TGA
CA SA	GAA	CTA	ATT	GAC	GGA	GTT	CTA	ဗ္ဗဋ္ဌ	ATA	ACA	AAG	TAT	GAG
ပ္ပ ပ္ပ	ACA	GAC	ACA	AAG	CAA	GAA	GIC	ATT	GAG	GAG	GGA	GAG	GAA
$_{ m LLL}$	GIT	ATT	GAA	GCA	ATT	ATG	GAA	\mathbf{LLL}	GTT	GAG	CIT	ATG	GTT
GAG	AAA	CIG	CCA	AAA	ACA	GAG	GGA	AAA	GAA	CAA	GGA	CAA	AGA
AAA	TTI	GTC	GAA	GGI	ATA	GAA	CIT	ATA	CAG	GLT	AAA	ATG	CCA
g C C	ggg	GTT	GTT	AGA	GAG	GTA	GTT	AGC	ACC	GAG	GTT	CCC	GCT
GGI	ggg	AGA	GTT	AAG	TTA	GAT	GTA	GAC	GAA	ATC	ATG	ATG	CIG
GAA	GAG	AGT	GAA	CTA	TIC	ATA	GTT	AGT	GGA	GAC	GAC	GAA	CTA
TTT	GAT	CCA	TAT	ATC	AAC	CTA	AAG	GTG	GAG	TTG	TCC	AAT	TTC
GTA	ATA	GAT	AAA	AAG	GAA	CCC	GCA	CTA	GCA	TTA	CIC	GGA	ACA
ATC	TTA	ATG	AGC	AAG	GAG	GTT	ACT	TCT	AAG	GGA	TAT	$\mathtt{T}\mathtt{T}\mathtt{I}$	CTT
GAA	AAG	ညည	\mathbf{LLI}	CTA	GGA	AGA	TTC	ပ္သင္ဟ	ATG	GAG	AGC	AAG	AGA
TTT	AGT	AGG	ATA	CAC	AAA	TTT	CCA	GAT	ATA	GAT	GTC	ATA	GGA
CCA	GCA	ATG	AGC	GAC	AAG	ACA	CTT	AAA	TLI	GAA	GGA	ACA	GAA
ATG	ACC	AGC	TCA	ATG	CIC	AGA	GAA	\mathtt{GTT}	GAA	CII	TAT	GTT	GAT

16 70 24 78 32 86

62

40 94 48

Figure 17FF

(PCNA) - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 33) Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 34) CGT (ALL POSSIBLE CODONS FOR ARGININE) GAG (ALL CODONS FOR GLUTAMIC ACID) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, V93E MUTANT: XXX = GAA,

162 216 270 324 378 432 486 540 594 648 CCG AAC ATA ACA CCA GCT AAT ACT GCA GAA AGA 999 CIC GTT TTA GCA CTC GAT GAA CTA AGC GAT GAT GGA ACC ACT GAC AGG AAG ပ္သင္ပ TAC ACA AAG AAT CIA AAA GCC AAG GTT ATA CIA GGA TAT GAA GAC ACA ATT GAG GGA GAG ACA AAG GAA ATT GAC GIC GAG CAA GAA GTT GCA ATG GAA TTT GIT GAG CIT ATG ATT ATT GAG GGA AGA CTGCCA AAA ACA GGA AAA GAA GA CAA AAA GAA GGT ATA ATA AAA GAA CAG GTT GTC CTT gag GTT GAG GTT GTT GLL AGC ACC GAG AGA GTA ggg AGA GTT AAG TTA GAT GTA GAC GAA ATC ATG ATG GAC GAA GAC GAA AGT CTA ATA GTT AGT GGA GAG CCA CTA GTG AAC AAT GAT ATC GCA AAG GAG TIG CIC ICC AAA TAT GGA ACA ATA GAA CCC CTA GCA TTA GAT CTT AGC TAT TTA ATG AAG GGA GAG GIT ACT TCT AAG TII AGA ggg AGC AAG TTTCIA GGA AGA TIC gg ATG GAG GIC ATA ATA AGT ATA TTTCCA AGG AAA GAT CAC GAT AGC AAG CCA GCA ATG GAC ACA CTT AAA $_{
m LLL}$ GAA GGA ACA GAA AGA GTT TAT AGC TCA GAA GAA GIT GAT ATG ATG CIC CTT

300 ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG GAGGCACGGG GAGACCAGTT CAAGCGCTAC CTTCTACGCC GGACAAGATA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC TTGAACCCTA TAACCGCCGA CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC AGTTCCTCGG CAGCGATAAG GATTGAGTAC GACCGGACTT CATTGAGGAA GTCAAGAAGA GTTCAGAAGA CAGGACXXXC GGTTGAAAAG TACTCATCCG GCGAGTTTAA CGGTTAAGCG AACTCTACTT ACGATTCTGC CTCCTGAAGG AAGGAAAACG GAGGTCTGGA CGAGAGCATC CTCATAGACA ACCGTTGTAA

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1440
                                                                                                                                   1020
                                                                                                                                                 1080
                                                                                                                                                               1140
                                                                                                                                                                             1200
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                                                                                                                    960
                                                                                                                                   CGGCCAGTCC
                                                                                                                                               CCTCAGGAAG
                                                                                                                                                                                            CGICICGCCG
                                                                                                                                                                                                           CGGCCACCGC
                                                                                                                                                                                                                                                                    AAGGGAGTAC
CCTTATGATA
                                                                         CTTCGATCTC
                                                                                                     AGCCTGGGAA
                                                                                                                    GGTCACATAC
                                                                                                                                                               GGCCAGAAGA
                                                                                                                                                                                                                         AGAGGAGAGG
                                                                                                                                                                                                                                        GCTCCTCGAT
                                                                                                                                                                                                                                                                                                 AAAGAAGGCT
                                                                                                                                                                                                                                                                                                                                                                          GGAGAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                       CGCGAGAGGA GTCAAATAC GCCCTGGAAC GGTGATAAGC
               TCTCCCCTAC
                             TGTGAAGGAG
                                                           CGAGCCGAAG
                                                                                        CGTTTATGAA
                                                                                                                                                                              GGAGAACATA
                                                                                                                                                                                                                                                        CGGCTATGCA
                                                                                                                                                                                                                                                                                    CTACAGCGAC
                                                                                                                                                                                                                                                                                                                                AGACGAGGAA
                                                                                                                                                                                                                                                                                                                                               GATAGCGAAA
                                                                                                                                                                                                                                                                                                                                                            GTGACGTCGA GAAGGCCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                      CGATACCGTT CGACGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG
                                             CTATCTGAAA
                                                                                                                                                                                                                                                                                                                 CGAGTACGAG
                                                                                                                                                                                                                                                                                                                                                                                         TCCCCACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTCCCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGGCIGAAG CCGAAGGGAA CT //TAG 2325
                                                                                                                                                                                                                                                                                                                                                                                                                                    TACTACATTG AGAACCAGGT
             GGCCAGGGTG ATAACTTGGA AGAACGTGGA
                                                                                                                                                                                                                                                                                                                               ATGCGGTGAT
                                                                                                                                                                                                                                                                    CGGCCTGGGG
                                                                                                                                                                                                                                                                                                 AAACCGTCAA
                                                                                                                                                                                                                                                                                                                                                                                        AGGCAACCGG
AGGGCCCAAT
                            TCCTCCGTGT
                                            TCGACTTCGC
                                                          GGGATGGAAG
                                                                         GACGGATACA
                                                                                       CGCTTGAGGC
                                                                                                     AAATAACCAC
                                                                                                                                 TCCGATGGAG GCCCAGCTTT CTCGCTTAAT
                                                                                                                                               CAGCACTGGC AACCTCGTTG AGTGGTTCCT
                                                                                                                                                                            GAGGGTTGTG
                                                                                                                                                                                            TCACCCACAA
                                                                                                                                                                                                           TATGACGTTG CCCCACAGGT
                                                                                                                                                                                                                         GAGACCICCI
                                                                                                                                                                                                                                        TCGAGAGGAA
                                                                                                                                                                                                                                                        ACGGTTACTA
                                                                                                                                                                                                                                                                                    TTAAGGTAAT
                                                                                                                                                                                                                                                                                                               CGCTTGAGCT
                                                                                                                                                                                                                                                                                                                                               GTGAGGCGTG ACTGGAGCGA
                                                                                                                                                                                                                                                                                                                                                                          AGCAAGTACG AGGTTCCGCC
                                                                                                                    AAGATGCGAA
                                                                                                                                                               AAAAGGAGCT
TGAGGCGAG GAGTTCGCCG
                                                                                                                                                                                                                                                                                                 GCCGATGCTG
                                                                                                                                                                                                                                                                                                                              AAGAAGAAGT
                                                                                                                                                                                                                                                                                                                                                                                          AAGGACTACA
                                                                                                                    TACTCGATGG
                                                                                                                                                                                            TCAATCATCA
                                                          GCCCTCGGAA
                                                                         GAAGTGAAGG
                                                                                       CCCACATACA
                                                                                                     TACGCTGAGG
                                                                                                                                                               AAGCCCGATG
                                                                                                                                                                                                                         AGCCTGCTTG
                                                                                                                                                                                                                                        ATTGACCCGA
                                                                                                                                                                                                                                                       GATCCTGGCA AACAGCTACT
                                                                                                                                                                                                                                                                                   GATAGAGGAA AAGTACGGCT
                                                                                                                                                                                                                                                                                                                CTTCCGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                      TGGGAGGATA GGCGACAGGG
                            GAGGGAGATG ATAAAGCGCT
                                                                                                                                                                            GAGCCCGAGA
                                                                                                                                                                                                                                                                    GAGAGCGTAA
                                                                                                                                                                                                                                                                                                                                                            CTAAAGGACG
                                            GGCGACAACT
                                                                                                                                                                                                           ATGCAAGGAA
                                                                                                                                                                                                                         ATTTATCCCG
                                                                                                                                                                                                                                                                                                                               CTTCGTCACG
                                            AACCTACAAC
                                                          AATAAACTTC
                                                                                                                                                                                           CCTGTACCCC
                                                                                                                                                                                                                                        GAAGGCCACG
                                                                                                                                                                                                                                                                    GGAGTGTGCA
                                                                                                                                                                                                                                                                                                                                             ACTTGAGATT
                                                                                                                                                                                                                                                                                                                                                                          CGAAAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                    CGACGCCGAG
                                                                                                     GGAGAAGGTT
                                                                                                                    AGTCGCCCGC
                                                                                                                                                               GGCCCCGAAC
                                                                                                                                                                             CTATGTAAAA
                                                                                                                                                                                                                                                                                                 AATACCTGGA
                                                                                                                                                                                                                                                                                                                                                                                          GAGGGATTTA
                                                                         GITIGCCGIC
                                                                                       GATAAACCTG
                                                                                                                                                                                                                                                                                                                CAACGCCAAA
                                                                                                                                                                                                                                                                                                                                                            TGAAGCTTTG
                                                         AAAAGCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGACAGGITG GITTGAGIGC
CTCTCTACCA
                                           ACGTTCTCAT
                                                                                                                                                                                                           ACAGAGAAGG
                                                                                                                                                                                                                         ACTTCCCAGG
                            TCTCGACGGA
                                                                         TGGGCGACAG
                                                                                                                                   AGGAGTTCCT
                                                                                                                                                                             ATGAAGGAGG
                                                                                                                                                                                           ATTTAGATC
                                                                                                                                                                                                                                        AGAAGAAGAT
                                                                                                                                                                                                                                                                                   CCATCAAGGA
                                                                                                                                                                                                                                                                                                 TTTTTGCCAC
                                                                                                                                                                                                                                                                                                                TCAAGTATAT
                                                                                                                                                                                                                                                                                                                                             CAACGCGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCACAAGTA
             ACGAGGAAGG
                                                                                                     GTCAGCCGAA
                                                                                                                    ACCTTGAGAG
                                                                                                                                               TCTCCCGCTC
                                                                                                                                                                                                                                                                                                                                AACGCGGCTT
                                                                                                                                                                                                                                                                                                                                                            CGAGGGTTCT
                                                                                                                                                                                                                                                                                                                                                                          AAGAAGTTAC
                                                                                                                                                                                                                                                                                                                                                                                                        AGAGGTTGGC
                                                                                      TAAGACGGAC
                                                                                                                                                               GGAATGAGCT
                                                                                                                                                                                                                                                       GGGCCATCAA
                                                                                                                                                                                                                                                                    GGTACTGCAA
                                                                                                                                                                                                                                                                                                                                                                                         AGCAGATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                      TCAAGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCTGAGAGC
               AGCTACGCCG
                                                                                                                                   GAGCTTGGGA
                                                                                                                                               CTCTGGGACG
                                                                                                                                                                                                            GATACGCTCA
                                                                                                                                                                                                                         TTCTGCAAGG
                                                                                                                                                                                                                                                                                  ATAACGATGA
                                                                                                                                                                                                                                                                                                                               GGCTTCTACA
                                                                                                                                                                                                                                                                                                                                                                          AGGATAGTCA
                                                                                                                                                                                                                                                                                                                                                                                       GTGATCCACG
                                                                                                                                                                                                                                                                                                                                                                                                       GCCGTTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                     TACATCGTGC
GACATTGAAA
                            GTTGACGTCG
                                            AAAGACCCGG
                                                         AAGCGCTGTG
                                                                        ATTCAGAGGA
                                                                                        TATCCTGTGA
                                                                                                     GCCGTCTTCG
                                                                                                                    ACCGGCGAGA
                                                                                                                                                               GCCTATGAGA
                                                                                                                                                                            CGGCAGAGCT
                                                                                                                                                                                            GTGTACCTAG
                                                                                                                                                                                                                                        CAGAAGATAA
                                                                                                                                                                                                                                                                   AGGCGCGCT
                                                                                                                                                                                                                                                                                                 ACCGACGGAT
                                                                                                                                                                                                                                                                                                                                             GGCAAGATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                    GACCCGACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTGAGAGAA
                                                                                                                                                                                                                                                       TACAGGCAGA
                                                                                                                                                                                                                                                                                                                ATGGAGTTCC
                                                                                                                                                                                                                                                                                                                                                            GAGACGCAGG
```

FIGURE 17GG

(PCNA) - Vent DNA POLYMERASE FUSION PROTEIN

// Nucleotide sequence (SEQ ID NO: 35) Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 36) Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) GAG (ALL CODONS FOR GLUTAMIC ACID) = GAA, V93E MUTANT: XXX

162 216 270 324 378 432 486 540 594 648 CCC AAC ATA ACA CCA GCT ACT GCA GAA AGA AAT TTA GCA GAA CIC CHC GAT CTA AGC GAT ATT GTT TAC ACC AAT GGA AAA AGG AAG ggg GAT GAG ATA AAG ACT GAC gcc ACA TAT GAG CAA GAA CTA GGA CTA AAG ATT GTTACA ACA AAG CAA GAG GGA GAG GAA GAC ATT GAA TII GIT ATT GAA GCA ATG ATG TII GTT GAG CLT GII ATT GAA GAG AAA CAA CTGAAA ACA GAG GAA CAA GGA AGA CCA AAA GGA AAA GGT ATA CCA ATA CAG AAA ATG GTC GAA GAA CTT GIT GCA GAG gg ggg GTT AGC GLT GTT AGA GTA GAG GCT GLT ACC AAG ပ္ပင္ပ GLT GAC GGT AGA TIA GAT GTA GAA ATC ATG ATG CIA GAG AGT GAC GAA CTA GAA AGT ATA GTT GGA GAC GAA TIC TAT CTA GAT CCA AAC AAG GIG GAG AAT TTC $_{
m LLL}$ AAG ATC GGA ATA GAT AAA GAA GCA CTA GCA ACA င္ပင္ပ AGC CTT ATC ATG AAG GAG GTT ACT TCT AAG GGA TAT TTT GAA AAG ggg TTICIA TTC ATG GAG AGC AAG AGA GGA AGA ggg GIC ATA GGA AGT ATA AGG ATA GAT CAC AAA CCA GAT GCA ATG AGC GAC AAG ACA CCA ACA CLL AAA TTT GAA GGA GAA GTT TCA ATG CTC AGA GAA GAA TAT AGC GII CTT GAT ACC

240 360 480 540 600 ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG TATATATGCT AAGGGAAGTT GAGACATGGA GGGCAAAATA TTTGCCGTAT AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA CAAGCGTTAT TGTTAAAGAA GTATCTCATA CCTTGCCTTT AATAATGATT TGCAGTGAAA GTCAGGAAAA AATTTTGGG TTCAGCCCTA TAAAGGGCGA CAGCTATGCG GAATTIGGAA AGGGCGAGAT AAAATATCGA TACCCTTTGC AGCTTAAGCT TTGTTCAAGT TTGATTTGCC TATTGAGGAG ATAAAGGCAA GAATATGACA GGAGACGAGG GGCCAGAGTA ATCACATGGA GACCCTCATT GGGGACAATT CAAGACXXXC ATAAAGCGTT AATAGAACTT TCCCATGGAG TGAGGGAGAT TGTCCAATGA AAGAGAAATG AACTTACAAT CGAGCATCCC TGACATTTAC ATGACTCCGC GAGTGCTCGA GGGAGTTTAA AGGGCTTGAT CGTTTTATCA ATGAAGAAGA ATGTGATAAT AGCTCATTTT CAGCTGTGGT AAACGGGCAG CTTCTCAAAG AGTTATGCCG AAAGAGAACG GAAGTCTGGA AAAGACCCCG AAAACTGTGA AGGGAACATC CTCATAGACA GTCGATGTTG GATATTGAAA

1500 1380 1740 1920 1980 1200 1260 1320 1440 2100 2220 1020 1080 1140 1560 1620 1680 1800 1860 2040 2160 TGAGGCAGTT GCTGATAGGT GTATCTTTA AGAGTATAAA AGGTTTGTGG TACTCACAAC TCCGATAGTA GGACTTAATT CGAAAAGAAA CGGCTATATG TAAGGTTCTT TGCAGTCATA TTGGAGTGAG AAGTGTTGAA ACCGGGCACA TTTAAGGTAT AATCCACTTT TGCCGCTATA TGCTAGGGCA CGCATGGGGG ACTCATTAAA GGTTCCACTT AGCCATTGGC AATTTTACTT GCTTGAGCTT AAACCAAGTT TCAAGGGTAG ACGATGTTGC ATAGAGGAAA AGTICGGCTI TTTGTTACAA AAAAGCGCTA ACTACATAGA CGTATACGCT CAGAGGAAAT CTGATGAGGA AGCCAGAAAA CCATACTCGG AAAAGCCTGA TAAGGAGAGA TTAAAGAGGG TAAAAGTGAA GCGATAGGGT GAAAGGAGGA CAATGGAAGA AGCTGGCAAA TCGTGGAGTG CAATAATAGT TTGACCCGAT ACAGCTATTA AAAGCGTTAC TTCCAGGTCT CAAAATACAG AGGACTACAA GGTAG 2325 GCTGTGGAAA CAGTIGIGG AAGGACGAIA AACCICCCAA TATGTAAAAG TGTAAGAATT AAATCCACAA TTGCTTGCAA ATACCCGGGG AACTCCAAAC TTGGAAGTAG GAGGCTATAC GAGAAAATAG GCAAGAGGGA GGAAAGATAA GATCCGGACT TTTGGATACA TGGCTCAAGA AAATTAGGAG ATGGAAGCTG ACCGGCAACC CCGAACAAAC CTGTACCCTT TTTATTCCCT GAATGTGCTG AGGGATTTAA GCCCAGTACT GAGATCAAGC CTTTCCGGGC GATAAGAGAA TTATGCCACA GAGAGGATTC TGATAGTTTT AACCAAAAGC ATTCTTCCCC TGAACTTGCA CCTGGGAGGA GAAGAAAATG GGCTATTAAA AAACTACATA AACAAGGGGC AGATGTTGTA GCAGATTACC AAGACTTGCC ACTCGAAGCG AACAAACCGG CTTAGATGCA GAAAAAACTA TTTCCGCAGT AAAAGAGGC GTACTCGAAG AAAGGTTTTA CAAAGGGAGC ATCCTAGAAA ACACAAGTAC ATACCCTTGA GCAGGATAAC AAGTTGTTAG TACTTAGGAT AGAGGATGGG TTTTAGGAAA AAGAAAGCAT TCGGGAAGGA TCTGCAAGGA CTGACGGCTT GCTTTTACTT AGACTCAGGC CGATAGCAAA GGGACGTCTC ACGCGAGGAA GAACAACTTA TTTATTTGGA AAGATATAAA ATAGGCAAAG AGGCAAGATG TAGAGATGAC AGGAATTCCT ATATCGTTCT TTATCCATGA CCCAAGATTC CAAAGCTCAA TATGAAGCAG TGGGAAACAG ACGTATGAGC AGGGTGGCAT GTATCCCCAG GGATATAGGT AGACACTACA TATGCGGACA ATAGCTAAGG AAAGCTGTAG ATAATAAGCT ACAGAATACG GATCTTTCC CGGCGCTTAA GAAAATATCA GCAATGAGGC GGGTATCCTA AAGAAAGCCA GAGTATGAGG GATGAAGAGG CCTCATGTCG TGCCGGCAG CAAAGTGTAT ATGCTCGATT GAAAAGCTTG

Figure 17HH

Vent DNA POLYMERASE - (PCNA) FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 67) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

1080 1020 1200 1260 1380 1440 1500 1560 1140 1320 1620 1680 360 540 600 999 840 900 960 AGAGTATAAA TATATATGCT GAGACATGGA AAGGGAAGTT GGCCAAAATA CAAGCGTTAT CCTTGCCTTT AATAATGATT TTTGCCGTAT ACATCCCGAA AATCCACTTT TGAGGCAGTT TGCCGCTATA TGCTAGGGCA GCTGATAGGT GTATCTTTTA AGGTTTGTGG TACTCACAAC TCCGATAGTA GGACTTAATT CGAAAAGAAA CGGCTATATG CGCATGGGGG TAAGGTTCTT ACTCATTAAA GCTTGAGCTT TGCAGTCATA CTATAATCCG AATTTTAAG TGTTAAAGAA GTATCTCATA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG CTGATGAGGA GAGAGGATIC TITGITACAA AAAAGCGCTA TTCAGCCCTA GGCCAGAGTA ATCACATGGA AAAATATCGA GGGACAAAGA TCAAGGGTAG CGTATACGCT AAAAGCCTGA TATTGAGGAG ATAAAGGCAA TAAAGGGCGA CAGCTATGCG TACCCTTTGC GGAGACGAGG AGCTTAAGCT TTGTTCAAGT TTGATTTGCC CAGAGGAAAT CAATGGAAGA AGCTGGCAAA TCGTGGAGTG AGCCAGAAAA TIGACCCGAT AAAGCGTTAC AGTICGGCTI AGGCCGAGAT CAATAATAGT ACGATGTTGC CCATACTCGG ACAGCTATTA TTCCAGGTCT CATAACAAA GATGGCAAGC CGAGCATCCC CAAGACXXXC TGACATTTAC GAATATGACA GAATTTGGAA TGTCCAATGA AAGAGAAATG ATAAAGCGTT GTCTTAGGAA GCTGTGGAAA CAGITGIGG AAGGACGAIA AACCICCCAA TTTTAGGAAA AACCAAAAGC AAATTAGGAG ATTCTTCCCC ATGGAAGCTG ACCGGCAACC CCGAACAAAC TATGTAAAAG TGTAAGAATT AAATCCACAA TTGCTTGCAA GATAAGAGAA ATAGAGGAAA TTATGCCACA ATACCCGGGG AGGAATTCCT AAACTACATA AACTCCAAAC GACCCTCATT GGGGACAATT GCCCAGTACT CTGTACCCTT GAATGTGCTG TTTATTCCCT GAAGAAAATG TCCCATGGAG TGAGGGAGAT AACTTACAAT AAAAGCTGGG AGTTCGGCTT TGATAGTTTT GAAAAAACTA GAGATCAAGC CCTGGGAGGA ATACCCTTGA AAAAGAGGGC GTACTCGAAG AATAGAACTT TTTCCGCAGT CTTTCCGGGC GGCTATTAAA TGAACTTGCA ATGATACTGG ACACTGATTA GGGAGTTTAA ATGACTCCGC CAGCTGTGGT AGGCTTGAT CGTTTTATCA ATGAAGAAGA ATGTGATAAT AGAGGATGGG AAGAAAGCAT TCGGGAAGGA GCTTTTACTT AGCTCATTTT GGGACGTCTC ACGCGAGGAA GAACAACTTA TTTATTTGGA AAGATATAAA ATAGGCAAAG TAGAGATGAC CTGACGGCTT TCTGCAAGGA AGGCAAGATG CTTCTCAAAG AAAACTGTGA GAAGTCTGGA AGGGAACATC CTCATAGACA GTCGATGTTG AAACGGGCAG CCCAAGATTC TATGAAGCAG ACGTATGAGC CAAAGTGTAT AGGGTGGCAT GTATCCCCAG AAGAAAGCCA GAGTATGAGG AAAGAGAACG AGTTATGCCG AAAGACCCCG **IGGGAAACAG** GAAAATATCA GCAATGAGGC AGACACTACA TATGCGGACA GATATTGAAA GATCTTTCC ATGCTCGATT GGGTATCCTA CGGCGCTTAA GGATATAGGT

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1920
                                 1980
                                                2040
                                                               2100
                                                                             2160
                                                                                              2220
                                                                                                               2280
               TTAAAGAGGG AAGTGTTGAA
  TTGGAGTGAG
                                GGTTCCACTT
                                                AGCCATTGGC
                                                                GCAAGAGGGA TAAAAGTGAA ACCGGGCACA
                                                                             GCGATAGGGT AATTTTACTT
                                                                                              AAACCAAGTT
                                                                                                                TTTAAGGTAT
TAAGGAGAGA
                               CAAAATACAG
                                              AGGACTACAA
                                                                                              ACTACATAGA
                                                                                                               GAAAGGAGGA
                                                                                                                             GG 2325 //
                                                                             GGAAAGATAA
                                                                                              GATCCGGACT
               AGACTCAGGC AAAGGTTTTA GAGGCTATAC
                                              AGGGATTTAA
                                                                                                              TACTIAGGAT ACTCGAAGCG TITGGATACA
                                                                                                                             AACAAACCGG CTTAGATGCA TGGCTCAAGA
  TTGGAAGTAG
                                 GAGAAAATAG
  GCAGGATAAC AACAAGGGGC
                                              GCAGATTACC
                                                              CGATAGCAAA AAGACTTGCC
                                AGATGTTGTA
                                                                             CAAAGGGAGC
                                                                                             ATCCTAGAAA ACACAAGTAC
                                 AAGTTGTTAG
                                               TTATCCATGA
                                                                             ATATCGTTCT
                                                                                                             TTGCCGGCAG
                                                                                                                             CAAAGCTCAA
  GATGAAGAGG
               ATAGCTAAGG
                               AAAGCTGTAG
                                              GAAAAGCTTG
                                                              CCTCATGTCG
                                                                             ATAATAAGCT
                                                                                             ACAGAATACG
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540
              216
                   270
                       324
                            378
                                432
                                     486
                                              594
                                                   648
         162
                                                       702
         CCG
                       ACA
                                     AAT
                   ATA
                            CCA
                                         ACT
                                              GCA
     GGG
                   TTA
              GTT
                       GCA
                                     GAA
                                          CTA
                                                       ATT
         CIC
                            CTC
                                GAT
                                              AGC
                                                   GAT
                                     AGG
                                          AAG
                                              AAG
                                                       TAC
     GAT
         AAT
              GGA
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                                AAA
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                                     ပ္ပပ္ပ
     GAA
                       GGA
                                          ATA
                                              ACA
                   GAC
                            GIT
                                 CTA
              ATT
     ACA
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                                         GAG
                                              GAG
              ACA
                        CAA
                            GAA
                                GIC
                                     ATT
                                                   GGA
              GAA
                   GCA
                                     TTT
                                              GAG
TTT
     GTT
                       ATT
                            ATG
         ATT
                                 GAA
                                          GTT
                                                   CTT
                       ACA
     AAA
                            GAG
                                     AAA
                                          GAA
                                                       CAA
                                              CAA
              CCA
                   AAA
                                 GGA
                                                   GGA
                                                             AGA
                       ATA
                                     ATA
              GAA
                   GGI
                            GAA
                                 CII
                                          CAG
GCA
    gcg
                       GAG
         GTT
              GTT
                   AGA
                            GTA
                                     AGC
                                         ACC
                                              GAG
                                 GTT
                                                   GTT
                                                            GCT
    ggg
                   AAG
              GTT
GGT
         AGA
                            GAT
                                     GAC
                                                  ATG
                        TTA
                                 GTA
                                          GAA
                                              ATC
                                                       ATG
    GAG
                   CIA
                                     AGT
                                                       GAA
         AGT
              GAA
                       TIC
                            ATA
                                GTT
                                         GGA
                                              GAC
                                                   GAC
                                                             CTA
    GAT
         CCA
              TAT
                                     GTG
                       AAC
                            CTA
                   ATC
                                 AAG
                                         GAG
                                              TTG
                                                   JCC
    ATA
         GAT
                   AAG
              AAA
                                                  CIC
                       GAA
                                GCA
                                              TTA
                            CCC
                                     CTA
                                         GCA
ATC
    TTA
         ATG
              AGC
                   AAG
                       GAG
                                ACT
                                         AAG
                                              GGA
                                                  TAT
                                                       TTT
                                                            CHI
                            GTT
                                     TCT
              _{
m LLL}
                                TTC
    AAG
         GCC
                   CTA
                                                  AGC
                                                       AAG
                       GGA
                                     GCC
                                         ATG
                                              GAG
                            AGA
                                                       ATA
         AGG
              ATA
                   CAC
                       AAA
                                CCA
                                     GAT
                                         ATA
                                              GAT
                                                   GIC
                            TII
    GCA
             AGC
                       AAG
                                     AAA
                                                       ACA
SCA
         ATG
                            ACA
                                CTT
                                         LLL
                                                  GGA
                                              GAA
                   GAC
                                                            GAA
             TCA
                                    GTT
         AGC
                  ATG
                       CIC
                           AGA
                                GAA
                                         GAA
                                             CTT
                                                  TAT
                                                       GTT
```

Figure 17II

Deep Vent- (PCNA) DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 37)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 240 300 360 420 480 540 600 99 720 780 840 900 960 1020 1080 1140 1200 1260 1320 1380 1500 1560 1620 1440 1680 1740 1800 CGATTATAAG GATTTTCAAG TTAGACCTTA CATTTACGCT GAGGCATGGG GAGGCCGATT GGATAAGATA GAAGAGGTAC GCTCGCATTT TATAATGATA TCTCCCGTAC GATAAGGGAG TGAGCCAAAG AGTTTATGAG GGCCTGGGAG GGTAACGTAC CCTCAGGAAG CGAGAGAAGG TAACGTCTCA TTATGGGTAC GGGGAGGGAA CTTATACATA AAAGAAGAAA GCTTGAGTAC GATAGATGAG CGAAATAGCC CTATCTAGTT CTTTGACCTC CGGCCAGCCC CTGGGAGGGG GGTTGGGCAC ATTGGATGAA GAAGATGCTT V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) TAACCGCCGA TAATCACCCA GCAAACAGCT ATTATGGGTA GGGGCTTGAA ATAGTCAGGA GGGACTGGAG AGTTCCTGGG CCGCAATAAG TICCGIICGC AGGGGCCCAT AAAAGATCGA TCCTCAAGGT GGGACGGTAG GAAGGATACA CCCTCGAGGC TACGCTCACG AGATAGCTGA TATTCAATGG AGGATGCAAA CAAGGTTAGT AGTGGTACCT AAGCCGGATG AGAGGGAGTA GGGATACGTT AAGGAGCCGG AGAAAGGGCT TCGCCCCAGA TCAAGAGGTT TTACGGCCTG CCGAGGAGAT TATAAACGCC AAGCTCCCAG GGCTGTTGGA TCGACCTTCC CAATCGAGAA GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GGCGATGAAG AGCTCAAGTT GGTTCAAAGT ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT GTTAGGAAGA GTAAGGAAGA CAGGACXXXC GAGTACGACA GAGTTCGCGA AGCCAAAGTC ATAACGTGGA GAGGGAGATG ATAAAGCGGT AACTTGGTGG CCCTCGATAA CCCAGCCTGC GAAAAGTTCG GGGCAAAAC GGCGATTCTT CCCCTGGGAA GCCCAGCTTT TCTAAAGACC GCAGAGAGCG V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, GAGATAAAGG CCAACATACA GAATACGATG GGCTGTACTT TGAACACCCT GGCTCCAAAC ATGACTCGCA GATTGATGAG TGCCGAAAAG CCGCAGTTAT TGACATCTTT CGAAGGGGAG GATAAACCTC TTCAACTGGC TCCAATGGAA TACCTACAAC GATAAAGCTA GACAGCGGTG GGAGAAAGTT AGTTGCAAAG CCCAATGGAG GAGCCTGTAC GGGGTTTATC GATGAAAGCT CAAAATCCTG CACAATTCCT AGGGTGTAGG TAAGGAGTGC GGAACTGGAG AAGGCCTAAT GACTGGAGAG TAATCACTAG ATGAGGAAGA TTTCCAGCGA ATGITATAAT AAAAGCTCGG TTGGGGGATAT GAAAGCCAAA GCTACGCTGG TAGATTTCAG TGAACAGGGA GTTGGTACTG ACGTGAGAGG GAATTATAGA CCCTCTATCA TTAGGAGAAC GGGAGTTCTT TTTCTAGGTC GGAATGAATT AGGACTTCCC AACGGGCAAT GACTCTACGC TCGTAGATTA TAAAAAGGAA TCGTAAGGAA GAAGGGAAGA CTCCTCAAAG CTAATAGACA GAGGTATGGA GTCGAGGTAG AAAGATCCCG GCCTACGAGA CTAAGGGAGA AAGTTCTGCA GATTACAGGC TATATAGAGT AAGATAGTGA GACATAGAAA AGCTATGCTG AAGAGGGCCG ATGCAGAGGC TACCACGTGA GCAATCTTCG ACTGGAAAGG GAGCTCGGTA CTGTGGGATG TTAGTTTCCC AGGCAAGAAA AGAGAGCATT CCGGATACGC GCAAAAGCCC GACACAGATG GCCCTAGAGT GAGGGCTTCT

								54	108	162	216	270	324	378	432	486	540	594	648	702		
1920	1980	2040	2100	2160	2220	2280	2328	GAC GAC	HTA	_	_	ATA							GAA	AGA :		
3CA	1AG	CAC	ATA	3AG	CCT	AAG		r ATA	r GGG		A GTT	TTA		CIC			CTA	3 AGC	GAT	: ATT	~	
GAG	GAA	CCG	GTG)	GAG	TTA(CAG		CTT	GAT	AAT	GGA		ACT		AAA		AAG	AAG	gcc	TAC	TGA	
TGAGGAGGCA	TCCAGAAAAG	AGGTCCGCAC	CATGGTGATA	TGCAGAGGAG	GGTTTTACCT	GTGGCAGAAG		CAA	GAA	CTA		GAC	GGA		CTA			ACA	AAG	TAT	GAG	
								ggg	ACA	GAC	ACA	AAG	CAA	GAA	GIC	ATT	GAG	GAG	GGA	GAG	GAA	
ATGGCAACGT	ACGAAATACC	ACAAGGCTAT	TGAGGCCTGG	GGGCTATCCT	TAGAAAATCA	AAGACCTCAG	// gy	TTT	GTT	ATT	GAA	GCA	ATT	ATG	GAA	TTT	GII	GAG	CTT	ATG	GTT	
ATG	ACG2	ACA.	TGAC	9999	TAGZ	AAG2	AGAAG	GAG	AAA	CTG	CCA	AAA	ACA	GAG	GGA	AAA	GAA	CAA	GGA	CAA	AGA	
AGC	AGT	AGT	AGG	AGA	ACA	AAG	AGA	AAA	$_{ m LLL}$	GIC	GAA	ggT	ATA	GAA	CTT	ATA	CAG	GTT	AAA	ATG	CCA	
ATCCTAAAGC	CTGAGCAAGT	CTTCACGAGT	GGAGTAAAGG	ATAAGCAAGA	GAGTATTACA	TACAGGAAAG	AACATCAAGA	GCA	gcg	GTT	$_{ m GLT}$	AGA	GAG	GTA	GTT	AGC	ACC	GAG	GTT	င္ပင္ပ	GCT	
	_	_				-	-	GGT	ggg	AGA	GIT	AAG	TTA	GAT	GTA	GAC	GAA	ATC	ATG	ATG	CTG	
GGCT	AAAG	gccc	TAGA	GCCA	CGCT	TGGG	GCTI	GAA	GAG	AGT	GAA	CTA	TIC	ATA	GIT	AGT	GGA	GAC	GAC	GAA	CTA	
CCTAGAGGCT	AACTGAAAAG	CACGAGGCCC	AGCCGCTAGA	AGACGGGCCA	GTATGACGCT	GGCCTTTGGG	GGCATGGCTT	TTT	GAT	CCA	TAT	ATC	AAC	CTA	AAG	GTG	GAG	TTG	TCC	AAT	TIC	
						_		GTA	ATA	GAT	AAA	AAG	GAA	CCC	GCA	CTA	GCA	TTA	CIC	GGA	ACA	
AAAG	GAGG	CAGA	AGGI	AGGG	CATA	TTAG	CTTA	ATC	TTA	ATG	AGC	AAG	GAG	GTT	ACT	TCI	AAG	GGA	TAT	TTT	CLI	
AAGCAAAAGT	TTAAGGAGGT	ACGAGCAGAT	CAAAAAGGTT	TGCTGAGGGG	GGAAGCATAA	GAATATTAGA	CAGGTCTTAC	GAA	AAG	ದ್ದಿದ್ದ	TTT	CTA	GGA	AGA	TIC	ပ္သပ္သ	ATG	GAG	AGC	AAG	AGA	
	-	•						TTT	AGT	AGG	ATA	CAC	AAA	TTT	CCA	GAT	ATA	GAT	GIC	ATA	GGA	
AAAGAAACCC	STAAAGATAG	TAGTTATT	PTGCCGTGG	SGGTACATAG	TCGATCTCA	SCCGTICTIA	ACTAAACAGA	CCA	GCA	ATG	AGC	GAC	AAG	ACA	CIT	AAA	TTT	GAA	GGA	ACA	GAA	
AAAG	STAA	CTAG	FTTG	3GGT	TTCG	3000	ACTA	ATG	ACC.	\GC	Ğ	\TG	ÜŢ	₹GA	3AA	TT	3AA	TT	[AT	J.T.	3AT	

Figure 17JJ

(PCNA) - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 37) Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 38)

FIGURE 17JJ (CONT.)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

54	108	162	216	270	324	378	432	486	540	594	648	702	
GAC	ATA	CCG	AAC	ATA	ACA	CCA	GCT	AAT	ACT	GCA	GAA	AGA	
ATA	ggg	CIC	GTT	TTA	GCA	CIC	GAT	GAA	CIA	AGC	GAT	ATT	
CTT	GAT	AAT	GGA	ACC	ACT	GAC	AAA	AGG	AAG	AAG	ပ္သပ္သ	TAC	:
CAA	GAA	CTA	ATT	GAC	GGA	GTT	CTA	ggg	ATA	ACA	AAG	TAT	GAG
ပ္သပ္သ	ACA	GAC	ACA	AAG	CAA	GAA	GTC	ATT	GAG	GAG	GGA	GAG	GAA
TTT	GTT	ATT	GAA	GCA	ATT	ATG	GAA	TTT	GTT	GAG	CIT	ATG	GTT
GAG	AAA	CIG	CCA	AAA	ACA	GAG	GGA	AAA	GAA	CAA	GGA	CAA	AGA
AAA	TTT	GTC	GAA	GGT	ATA	GAA	CIT	ATA	CAG	GTT	AAA	ATG	CCA
GCA	ggg	GTT	GTT	AGA	GAG	GTA	GIT	AGC	ACC	GAG	GTT	ပ္သ	GCT
ggT	ggg	AGA	GTT	AAG	TTA	GAT	GTA	GAC	GAA	ATC	ATG	ATG	CTG
GAA	GAG	AGT	GAA	CIA	TIC	ATA	GTT	AGT	GGA	GAC	GAC	GAA	CIA
TTT	GAT	CCA	TAT	ATC	AAC	CTA	AAG	GTG	GAG	TTG	TCC	AAT	TIC
GTA	ATA	GAT	AAA	AAG	GAA	CCC	GCA	CTA	GCA	TTA	CIC	GGA	ACA
ATC	TTA	ATG	AGC	AAG	GAG	GTT	ACT	\mathbf{ICT}	AAG	GGA	TAT	TTT	CII
GAA	AAG	ပ္သပ္သ	$_{ m LLL}$	CTA	GGA	AGA	$_{ m TTC}$	ပ္သင္ဟ	ATG	GAG	AGC	AAG	AGA
TTT	AGT	AGG	ATA	CAC	AAA	TTT	CCA	GAT	ATA	GAT	GIC	ATA	GGA
CCA	GCA	ATG	AGC	GAC	AAG	ACA	CTT	AAA	TTT	GAA	GGA	ACA	GAA
ATG	ACC	AGC	TCA	ATG	CTC	AGA	GAA	GTT	GAA	CTT	TAT	GTT	GAT

9	120	180	240	300	360	420	480	540	900	099	720	780	840	900	960	1020
GATTTTCAAG	TTAGACCTTA CATTTACGCT	GAGGCATGGG	GAGGCCGATT	GGATAAGATA	GAAGAGGTAC	GCTCGCATTT	TATAATGATA	TCTCCCGTAC	GATAAGGGAG	CTATCTAGTT	TGAGCCAAAG	CTTTGACCTC	AGTTTATGAG	GGCCTGGGAG	GGTAACGTAC	CGGCCAGCCC
ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG	TTAGACCTTA	GTTAGGAAGA TAACCGCCGA GAGGCATGGG	TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT	TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA	TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC	CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT	GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT	ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA	TITCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG	AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT	AAGAGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG	ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC	CCAACATACA CCCTCGAGGC AGTTTATGAG	TACGCTCACG AGATAGCTGA GGCCTGGGAG	TATTCAATGG AGGATGCAAA GGTAACGTAC	GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC
GATGGGAAGC	GACAGAAACT	GTTAGGAAGA	GTAAGGAAGA	CAGGACXXXC	GAGTACGACA	GGCGATGAAG	GAGTTCGCGA	ATAACGTGGA	ATAAAGCGGT	GGCGATTCTT	CCCCTGGGAA	GAGATAAAGG		TACGCTCACG	TATTCAATGG	GCCCAGCTTT
CATCACCGAG	GGTTGAGTAC	GATTGATGAG	TGCCGAAAAG	TGAACACCCT	TGACATCTTT	TCCAATGGAA	CGAAGGGGAG	AGCCAAAGTC	GAGGGAGATG	TACCTACAAC	GATAAAGCTA	GACAGCGGTG	TTAGGAGAAC GATAAACCTC	GGAGAAAGTT	AGTTGCAAAG	CCCAATGGAG
ACGCTGACTA	AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT	CTCCTCAAAG ATGACTCGCA GATTGATGAG	AAGATAGTGA GAATTATAGA	GAGGTATGGA GGCTGTACTT	AGAGAGCATT CCGCAGTTAT	AAGGCCTAAT	CCCTCTATCA			ATGTTATAAT	AAAAGCTCGG	TTGGGGATAT	TTAGGAGAAC	GCAATCTTCG GAAAGCCAAA GGAGAAGTT	ACTGGAAAGG GACTGGAGAG AGTTGCAAAG	GGGAGTTCTT
ATGATACTTG	AAAGAAAACG	CTCCTCAAAG	AAGATAGTGA	GAGGTATGGA	AGAGAGCATT	CTAATAGACA	GACATAGAAA	AGCTATGCTG	GTCGAGGTAG	AAAGATCCCG	AAGAGGGCCG	ATGCAGAGGC	TACCACGTGA	GCAATCTTCG	ACTGGAAAGG	GAGCTCGGTA

REPLACEMENT SHEET

FIGURE 17JJ (CONT.)

CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TAGTTTCCC	TAGATTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGICICA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
SATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAACTGGAG	GAAAAGTTCG	GGTTCAAAGT	CTTATACATA	1620
SACACAGATG	GACTCTACGC	CACAATTCCT	GGGCCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
SCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
SAGGGCTTCT	ACGTGAGAGG	GTTCTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
SAAGGGAAGA	TAATCACTAG	GGGCCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
STAAAGATAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
STIGCCGIGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100
SGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220
SCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17KK

JDF-3 - (PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 67)

FIGURE 17KK (CONT.)

CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) CGG, CGA, CGC, = AGA, AGG, V93R MUTANT: XXX

CAGGTCTGTGGAGGTCTTGGGTCCTCTACTTCACGCACCCGCAGGACXXXCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGGGTCATCGACATCTACGAGTACGACATACCC ttcgccaagcgctacctcatagacaaagggcctaatcccgatggaaggtgaggaagagcttaaactcatgtccttcgadatdGāGacgctctaccacgaggagaagagtttggaa **ACCCTCGGGACGGGACGCGAGGCGGAGATACAGCGCATGGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTTCGACCTTTATCCAGTCATAAGGCGCACCATAA** ACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACGCGGCGAGGGGGCTTGAGAG асвесветвестасетсалевавссвелествтвеваслатитсететатетатета дептеста в стетет построват са поста с поста поста п gaactogaatacgaggcttctacgtcaggggcttcttcgtcacgaagaaaaagtacgcggtcatcgacgaggagggcaagataaccacgcgcggggcttgagatagtcaggcgcg ACTGGAGCGAGATAGCGAAGGAGAAGCGCAGGCGTTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAAATTGTCAGGGAAGTCACCGAAAAAGCTGAGGAAA GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAGGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAGCGTTTGGCCGACAGAGT GITAAAAICCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGACGAAGCACAAGTACGATG CGGACTACTACTACGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGC GCGCTTCTTGAGGGTCGTTAAGGAGGACCCCGGACGTGCTGATAACATACAACGGCGACAACTTCGACTTCGCCTACCTGAAAAACCGCTGTGAGAAGCTTTGGCGTGAACTTTT GGTCGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCC CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAATCTCCTTCGATTACAGGCAACGGCGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT ATGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAAGTACATCGAAATGGTCATCAGAGAGGGGAAAAGTTCGGTTTTAAAGTCCT CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAAAAGGTCAAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCCTTCTC ATGATCCTTGACGTTGATTACATCACCGGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAGAGGGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCTTCTTCT GTGGCTGAAGCCGAAGGGGAAGAAGAAG//

162 216 270 324 378 432 486 540 594 CCG AAC ACA CCA GCT AAT ACT GCA GAA GGG ATA TTA ATA ATA GCA CTA AGC CTC CIC GAT GAA GAT AAG TIT GCC CAA CIT AAT ACC ACT AAA AAG ggg GAT GGA GAC AGG ACA GAA CIA GAC GGA CIA ATA AAG GLL ggg ATT GAG GAG ACA GGA GAC ACA AAG CAA GAA GIC ATT GTT GAG ATT GAA GTT GAA GCA ATT ATG TIT CTT GAG AAA ACA GAG GGA CIG CCA GGA AAA GAA CAA AAA GGT GLT AAA GTA TIT GAA GGT GCA AAA GCG TTT GIC GAG ATA GAA ATA GAA CII CAG GTT GTA ACC GAG GIT GTT AGA GTT AGC ပ္သပ္ပ ATC ATG AAG GAA AGA GTT TTA GAT GTA GAC GAC ATA GAT GAG GAC CTA TIC GAA GIT AGT GGA CCA AGT CTA ATA TAT GAA AAC TIG JCC GAG AAG ATC GCA AAG GTG GAT AAA CCC CTA TTA GCA GAA ATC TTA TAT ATG AGC AAG GAG GGA GII ACT TCT AAG ပ္သင္ပ ATG GAG AGC AAG $_{
m LLL}$ CIA GGA AGA TIC ggg TTTAGT AGG ATA AAA CCA GAT GAT CAC TTTGCA ATG AAG CCA GAC ACA TTT GAA AGC CTT AAA GGA ACC AGC CIC AGA GAA CII TCA ATG GTT GAA TAT

FIGURE 17KK (CONT.)

702 GIT ACA ATA AAG TIT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC AIT AGA GAI GAA GGA AGA CIT ACA ITC CIA CTG GCI CCA AGA GIT GAA GAG TGA

Figure 17LL

(PCNA) - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 39) Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

54	108	162	216	270	324	378	432	486	540	594	648	702	
GAC	ATA	റ്ററ്	AAC	ATA	ACA	CCA	GCT	AAT	ACT	GCA	GAA	AGA	
ATA	999	CTC	GTT	\mathtt{TTA}	GCA	CIC	GAT	GAA	CTA	AGC	GAT	ATT	
CTT	GAT	AAT	GGA	ACC	ACT	GAC	AAA	AGG	AAG	AAG	ggg	TAC	:
CAA	GAA	CTA	ATT	GAC	GGA	GTT	CIA	ggg	ATA	ACA	AAG	TAT	GAG
ggg	ACA	GAC	ACA	AAG	CAA	GAA	GTC	ATT	GAG	GAG	GGA	GAG	GAA
$_{ m LLL}$	GTT	ATT	GAA	GCA	ATT	ATG	GAA	TTT	GLT	GAG	CLT	ATG	GTT
GAG	AAA	CIG	CCA	AAA	ACA	GAG	GGA	AAA	GAA	CAA	GGA	CAA	AGA
AAA	$_{ m TTT}$	GTC	GAA	ggT	ATA	GAA	CTT	ATA	CAG	GTT	AAA	ATG	CCA
GCA	පුදුල	GTT	GTT	AGA	GAG	GTA	GTT	AGC	ACC	GAG	GIT	CCC	GCT
GGT	ggg	AGA	GTT	AAG	TTA	GAT	GTA	GAC	GAA	ATC	ATG	ATG	CTG
GAA	GAG	AGT	GAA	CTA	TIC	ATA	GIT	AGT	GGA	GAC	GAC	GAA	CTA
TTT	GAT	CCA	TAT	ATC	AAC	CTA	AAG	GTG	GAG	TIG	TCC	AAT	TIC
GTA	ATA	GAT	AAA	AAG	GAA	CCC	GCA	CTA	GCA	TTA	CTC	GGA	ACA
ATC	TTA	ATG	AGC	AAG	GAG	GTT	ACT	TCT	AAG	GGA	TAT	TTT	CTT
GAA	AAG	ggg	$_{ m TTT}$	CTA	GGA	AGA	TTC	ပ္သင္ဟ	ATG	GAG	AGC	AAG	AGA
TTT	AGT	AGG	ATA	CAC	AAA	TTT	CCA	GAT	ATA	GAT	GTC	ATA	GGA
CCA	GCA	ATG	AGC	GAC	AAG	ACA	CTT	AAA	TTT	GAA	GGA	ACA	GAA
ATG	ACC	AGC	TCA	ATG	CIC	AGA	GAA	GTT	GAA	CTT	TAT	GTT	GAT

gacarctacgagracgacaracccrrcgccaagcgcraccrcaragagcaagggccraarcccgarggaaggrgaggaaggcrraaacrcargrccrrdgagardga CTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGGAGAAGGTGA AGAAAAGTTCCTCGGCAGGTCTGTGGAGGTCTTGGGTCCTTTCACGCACCCGCAGGAC<u>XXX</u>CCGGCAATCCGCGACAAATAAGGAAGCACCCCGCGGTCATC ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCC

FIGURE 17LL (CONT.)

AGCGGGGACTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTCAACCTTCAATCATAATCACCCACAACGTCTCGCCAGATACGCTCAACCGCGAGGGGTGT GAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGATTACAGGCAACGG<mark>GCG</mark>ATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATG GCACGTAGCCATAGCGAAGGGTTTTGGCCGCCAGAGGTGTTAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAAGG CGATTCCCTTCGACGAGGTTCGACCCGACGAGGAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGC CTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATACAACGGCGACAACTTC CGAGGTGAAGGGCAGGGTACACTTTCGACCTTTATCCAGTCATAAGGCGCACCATAAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGC CCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAGAGGGTCGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAG CTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCCCGGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCCT AGGAGCTACGACGTTGCCCCCGGAGGTCGGTCACAAGTTCTGCAAGGACTTCCCCGGCTTCCATTCCGAGCCTGCTGGAAAACCTGGAAGAAAGGAAAAGGCAGAAGATAAA CCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGGGGTTGAGGAAAAGTTCGGTTTTAAA GTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACT GCCCGGCCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAAGTACGCGGTCATCGACGAGGAGGGGCAAGATAACCACGCGCG GGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGCAGGCGAGGCGATTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAATT TACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGCGTGGCTGA

Figure 17MM

Sac7d gene (ACCESSION No: M87569)

Nucleotide sequence (SEQ ID NO: 69) Amino acid sequence (SEQ ID NO: 70)

36 108 67 201 54 162 D GAC L TTA M V K V K F K Y K G E E K E V D T S ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAA GAA GTA GAC ACT TCA K I K K V W R V G K M V S F T Y D AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC N G K T G R G A V S E K D A P K E AAT GGT AAG AGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA L D M L A R A E R E K K * TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA TAA

Figure 17NN

Sac7d-Taq DNA polymerase fusion protein

Amino acid sequence (SEQ ID NO: 70) // Amino acid sequence (SEQ ID NO: 66) Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 65)

M V K V K F K Y K G E E K E V D T S ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAA GAA GTA GAC ACT TCA

D GAC AAG ATA AAG ATT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC N G K T G R G A V S E K D A P K E L AAT GGT AAG GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA

V GTG T ACC A A A P CCA P ი მგმ L K AAA Y T ACC L CTC r CTG A GCC T ACG CTG s AGC DGAC CA GA ය ශීශීශී r CTC CIC K AAG CCC CTC D GAC CHC A GCC **A** 0000 E V GTC ဗ ၁၅ s AGC **₽** A GCC D GAC L CTG ACC GGG CGG CCC CTC GGG K AAG AAG D GAC CGG V GTG V GTC CAC R AGG K G AAG GGC IATC LCTG A GCC ဗ္ဗဋ္ဌ r CTG DGAC $\dot{\mathbf{F}}$ L CTG z :: K K AAG AAA A GCC F V GTC A GCG E D GAC GGC R v GTC දි අ Ω CAC ව වූ V GTG K AAG A GCG V GTC မ ည K AAG CAC Y TAC Y E I E GAG IATC GAG E F Y TAC I ATC K AAG A V GCG GTG G Y R T CGC ACC A V GCG GTC Y TAC R AGA F TTT ဗ ဗ္ဗ r CTC සි උදි E GAA Ω CIC. ა უ gcc ဗ္ဗဋ္ဌ W GAA GAA DGAC Q CAG E GCA DGAC ကို ည Y Y TAC L PCCG s TCC L r AGA A GCC ი მვვ A GCC V GTC k AAG r CTG caa Caa ₩ TGG V GTG L ы E D GAG GAC (L CTG gca Bca P E GAA M ATG E GAG E GAG A GCC ස ප r CHC ø S G AGT GGG A CAC H CTC A GCG L D M L TTA GAC ATG TTA E က် ကိ CAG CAG P CCG g GGT œ K AAG CAC g GGG ය පු R CGC k AAG F TTT Y ACC ဗ ဗိဗ္ဗ × V T GTC ACT CGG CTC) 299 // 9 ი ენ F D GAC K AAG I ATC A GCG L Ω A GCC CIC D GAC s AGC S TCC GCC DGAC E CTG

GAA $^{\rm L}_{\rm CTG}$ D GAC 8 3 3 3 4 8 A 200 **A** 2300 CIG ı H r GTT A g GGC F Y K TAT AAA V GTT CIG R R G G ය ය ဗ္ဗဗ္ဗ r CTG CIC I ATC T Y r DFD K AAG LCTT S AGC s AGC R E GAG F E GAA CIC r CGC R AGG CCC ი წვვ E V GTG D GAT CCT R GG E P CCG r CTG M ATG සු පු CTTE GAG DGAC CCC ₩ TGG ස උදු K AAG DGAC CAC ු වි A GCC g G G A P GCC CCC (A K GCC AAA GAG TCC GAC AAC . E I ATC A GCC မှ ည CTC မှ ငြင် W TGG GAC V GTG LCTT D GAC (GAG M ATG A GCC L CTG E CTC TGG ი ცვვ gcc Bcc ය විවි L r CTG မှ ငြင်င D GAC R CGG s AGC ပို့င္ပင္ ပ္ ပင္ပ ကို ည E **₽** ဗ္ဗဗ္ဗ H CAC CTT K AAG W TGG R AGG gac Gac L CTT P CCC CCC E GAG GGG L S CTC TCC r CTG K AAG or CTC ව විව K AAG E GAG P CCG ACC. ACC GGG GAC K AAA F TTT E R CGG GGG R A GCC GAG cgc Cgc ACC R AGG ස විවි CIC E ය ශ්රී A GCG DGAC K AAG F LCTT r CTG S TCC ය ගියි A GCG ය ය N AAC R G AGG GGG (CTG E GAG TACG r CTG DGAC A CCC s TCC r r Agg L E GAG r CH K AAG K AAG ටටල ඉහට D GAT k AAG N AAC V GTG E V GTG တ္မင္သင္သ CCT GAG E R AAG D GAC L GCC F TTT gcc Gcc r CTG DGAC E GAA ი მვვ L CTC DGAC M ATG L CTG F s AGC ය ය A GCC R AGG r CTG TGG L R CTC AGG 3CC GAC IATC L CAC မှ A GCC GAA V GTG A CIG CTC E GAG CTG . ဗ္ဗဋ္ဌ A GCC R AGG F A GCC L CTG r CTG A GCC

N AAC IATC T ACC Y TAT A GCC ACG S AGT R AGG V 3TG I ATC I ATC E CTC Y A GCC GAG r CTC R AGG r CTA D GAC සි සි o CAG M ATG r CTG LCTT E N AAC ပို့ မှာ r CTG EGAG CCC CTG N AAC W TGG ACG R RGG ი მმც ¥ TGG A GCC A GCC F L V GTC R CGG H CAC g GGC CTT A D EGAG s AGC ကို ည I ATC g GCC L EGAG V GTG ව විරි A GCC Y TAC T ACG ල වි V GTG D GAC R L AGG CTC E H o CAG CTC ဗ ဥဌ M ATG r CTA A GCC A GCC T ACC L TTG H T E T CAC CAC ACG GAG ACC CAC L CTG E ဗ္ဗ s AGC $_{
m L}$ DGAC T ACG GGC GGC LCTA s TCC S A GCC DGAC V GTC W TGG A GCC T ACC I CCG ₽ GCC CTC K AAG r TTG E GAG L CTG F TTT S TCC ACG ය ශීශී CAC L TTG L CTG ကို ည D I GAC ATC (V E GTG GAG ი გგ ය වූ CTC R CCC CAG IATC E A GCC v GTC A GCC E GAG F orc . N AAC R AGG K AAG D GAC N AAC CIG A GCT E I ATT r CTC V GTC r Agg ဗ္ဗဗ္ဗ I ATC \mathbf{F} CAG **₽** V GTG r GTT s TCC CGG ი გგე Y LCTT Y TAT E GAA CCC E T ACC GGC R CIC I ATC r AGG R AGG Q E A GCC **₽** K AAG CAC ი მვი ۳ کی $_{
m L}$ T ACC T ACC N AAC FTTC CIC V GTG САС E GAG CAG A GCC GGC P A GCC TGG R AGG E GAG s AGC GAG DGAC A.A.G DGAC E CTC DGAT FTTC E r CTC ACG සු පු I ATA A N GCC AAC V GTC V GTG r CTG ස උදි R CGG K AAG CTG CAG CAG င်ရှင် සි දි S TCC အင္ E န Tcc ဗ္ဗဗ္ဗ CTC K AAG ဗ ဗ္ဗ s AGC IATC GGC **A** 200 S AGC

P 200 Y V GTG ဗ္ဗဋ္ဌ E A ₽ 200 **0** ACC ය ශීශීශී ය දි CAG E GAG r CTA F LCTG EGAG v GTC R AGG CTC K AAG GAG S AGC K CGG L E A CTA GAG GCC M ATG CCC F N M P TTC AAC ATG CCC V GTC V GTC A GCC CAG CAG CAG R AGG ሷ R AGG FA GCG S TCC F TTT L E E G GAG GGC A Y V P D TAC GTG CCA GAC GGG L E K AAG CTC Y V K GTG AAG C DGAC R GGC င် င်င်င A GCC M ATG E ₽ GCC CAC CAC E L CTG CTG (M ATG L CTG M ATG V GTC A GCC I ATT R CGG E K T GAG AAG ACC R P යිදු A GCT CAG A GCC s TCG F r CTG (D GAC R CGC E GAG L MATG V GTG A GCC K AAG V GTG CGC යියි CAG A GCC CIC A GCC MATG A GCC I ATT g GGC A GCG Y A GCC M ATG E GAG A W GCC TGG L F CTC TTC (D L GAC CTC / E E r CTC E R AGG A GCG යියි V GTC E R CGG A GCC R AGG T ACC P r CGG V GTG A GCC ი მმმ Y ව පිරි E V E GTG GAG V GTC s AGC A GCC M ATG F V GTG AAA PCCT K AAG ဗ္ဗဗ္ဗ NAAC K AAG T ACC I ATC GAA GAA CCA W TGG GAC CAT GAG H ი ცვვ H I ATA ව පුර ი მვვ စ ဗ္ဗ GGC GGA (GTG > GAG ы GGC BC v GTG L E CTG GAG စ ဗ္ဗ DGAT CCC I ATT V GTG ဗ ဗ္ဗ ggg E Ø L K AAG CCC A GCC TAT S TCC × V GTG CIC

H H * CAT CAT TAA

Taq DNA polymerase- Sac7d fusion protein

Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 70) Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 69)

9 6 G // GGC GGT

V GTG T ACC K AAG D K GAC AAA PCCC CCA ი გე L V T S G M L P L F E P K G R V L L GTC ACT AGT GGG ATG CTC CTC TTT GAG CCC AAG GGC CGG GTC CTG r CTC D G H H L A Y R T F H A L K G L T GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC A CCC L CTG S AGC T ACG GGG GAG CCG GTG CAG GCG TAC GCC AAG AGC CTC V L A GTC CTG GCC D A V I V V F D A K GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG Y G G Y K A G R A P TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC V D L GTG GAC CTC A K K A E K E G Y E V R I L T A GCC AAG AAG GAG GAC TAC GAG GTC CGC ATC CTC ACC GCC D D GAC GAC E L GAG CTG A L I K GCC CTC ATC AAG G Y E A CTC P CCG g GGG A GCC CA O V GTC H E L E K E D AAG GAG GAC R CGG r CCC R GGC R CGC $_{
m TTT}$ S R AGC CGG (A L GCC CTC 1 S F TCC TTC L A CTG GCG E D GAG GAC

r CTG DGAC CTT CTT A GCC A A GCC r Fg K AAG EAA V GTC L CTG IATC T ACC R AGG စ ဗ္ဗ ი მემ A A A V GTT L CTC စ ဗ္ဗ CAG A A A A G CIC ი მმ s AGC GGC BC E GAG F E GAA Y TAT S AGC GAC CIT EGAG M ATG (GAG CCG V GTG GAG P CCT CCC P CCC မှ ည ი მგ CGG D GAT CIG TGG GGG R CCG ပိုင္ပဲ CAC K AAG H A GCC E GAG DGAC R AGG LCTT GAC GGC CTG A I GCC ATC D GAC AAA AAA V L GTC CTC CCC CCC gcc Ccc GCC CCC r CTC ကို ည W TGG S D N TCC GAC AAC GAG GAG ш G D GGC GAC C GCC c_{TG} E GAG r CHO TGG M ATG A GCC 囮 GCC CCC R CGG r CTC Y r CTG DGAC S AGC ပိုင္ပဲ ကို ည ස පු W E K TGG GAA AAG 1 E GAG K AAG S D R I TCC GAC CGC ATC L ₩ TGG ဗ္ဗင္ဗ CAC CIT GCC CCC r Agg A GCC E GAG A K GCC AAA GCG D L CTG န ၂୯୯ \mathbf{F} E GAG AAG V GTC g GGG E K T A R K GAG AAG ACG AGG AAG T G ACC GGG G CGG R R CGG CIC CIC E GAG R စ ဗ္ဗ L D CTG GAC LCTT $_{
m L}$ ₽ GCG A A A G F r CTG s TCC စ ဗိမ္မ CTT TGG L CTG crg GAC ი მემ E GAG L r Agg A GCC CTT L K CTG AAG Q L CAG CTC (P A CCG GCC ' ဗ ဗ္ဗ A GCC N AAC D GAT E K AAG V GTG V GTG R AGG GAA (AAG. R CGG L CTG GAC E GAG CCC F TTT **₽** L R CTG AGG Y TAC T ACC CTC r CTG Y ი გე DGAC M ATG F TTT s AGC ဝ ၁၁၅ A GCC D L GAC CTT' L I CTC ATC L R CTC AGG GAC I ATC CIC CAC CCC GAA V GTG A GCC A GCC r CTG F CTG ဗ္ဗဗ္ဗ A GCC A GCC A GCC r CTG R AGG

T ACC I ATC N AAC IATC A T ACG R AGG F ස වි V STG S AGT EGAG r CTC ₽ GCC CIC E r GFC Y ဗဗ္ဗ R AGG CTA CAG N AAC CCC L CTG E E GAG ය පු R AGG CIT ACG P CCC R AGG F GGG GAG TGG **₽** A GCC CTT d GTC යියි CAC ရှင် ၁၁၅ r CTT E CCC gcc Bcc Y TAC A GCC s TCC CTT V GTG ი მ<u>ვ</u>ვ I ATC T ACG P E GAG CAC CTA A GCC o CAG V GTG CTT ч Б M ATG CTC A GCC T ACC L E GAG S AGC ი ცვვ gcc Gcc R AGG CAC ရ ဝင္ပင L CTG D GAC T ACG r CGC ы S T TCC ACC I ATC **&** 22 s TCC **₽** DGAC V GTC GAG A GCC CCG A GCC E AAG r TTG r CTG F TTT ကို ည සි දි GAG r CTG r TTG TACG P CCC Ö A GCC R r CTC GGC BBC E GAG CCC CAG ACC GAG ი მმმ V GTC I ATC 闰 L R CTC AGG (K AAG F V GTC V GTG ACC E GAG DGAC N AAC ი მც A GCT N AAC E R GAA AGG T G ACC GGC N AAC I ATC gCG န Tcc V GTC I ATT F CAG CAG CTT s TCC Y TAT E P CCC E GAG LCTT R AGG Y TAC မှ ၁ CTC E K GAG AAG V A GTG GCC A GCC L CTG E GAG CAC N AAC CCT ი მმმ ကို ည T ACC ACC CAC CAG GAC ACG GAG A GCC ¥ 8 R AGG s AGC CCC Þ K AAG CIC ₩ TGG GAG GAC CTC D GAC ACG E r CTG D GAT အင္လ යියි K AAG CIC E N AAC V GTG r CTG R CGC CIG အင္တ s TCC Y ე შვ g G C C GGC PR A GCC s TCC ဗ္ဗဗ္ဗ r CTC S AGC GAG K AAG ဗ္ဗဋ္ဌ

Y I ATC A မှ ည V GTG ဗ္ဗဋ္ဌ E F IATC A GAC r CTG ACC. CIA CAG r CTG E M ATG F ပ ပ္ပ R GGG E CTG N AAC W k AAG E S AGC A GCC V GTC R AGG r CTC ස විව M ATG GTG GCC က် ည E s AGC **₽** CAG CAG R AGG E မှ ည V GTC V GTC DGAC R AGG L F GAG ₽ GCC gcg G S TCC F TTT M ATG CIG F N TTC AAC Y TAC D GAC CIC K AAG GGG TGG CTA TTG စ္မွင္မ T ACC GGG R r CHC ဝ ဝိဇ္ဇင E K AAG S TCC CCA E င္ပင္သင GGC By GGC GAG DGAC A GCC V GTG V GTG H CAC E E မှ ၁၁ CAC GG T ACG M ATG CIG CAC r CTG M ATG CAC A GCC I ATT CIG Y TAC M ATG V GTC යි දි D I GAC ATC GCC CCC T ACC සි CGC BC A GCT CAG CAG ggc G S TCG F **₽** TTC ATC GCC GAG GAG GAG LCTG L CTG D GAC M ATG **A** GCC K AAG සි CTT V GTG K AAG V GTG CGG ဗ္ဗဗ္ဗ CAG GAG r GGC A GCC v GTG r Gid ₽ GCC D L M GAC CTC ATG A ¥ TAC A GCC I ဗ္ဗဇ္ဗင A GCG R AGG ი წვვ gcc Gcc E M ATG R E CGG GAG (CIC F E GAG E GAG ₩ TGG CTC E R AGG A GCG ပ္သင္ဟ E E A GCC L O CAG R CGG V GTC A GCC R AGG 990 A GCC I ATA Y ස දු T ACC ი ცვი F P CCC ი მწმ V GTG GAG K S AAG AGC ATC CGC F A GCC M ATG Q CAG v GTC V GTC CCT V GTG E GAG K AAA T ACC I ATC V GTG s AGC ဗ္ဗဗ္ဗ N AAC K AAG E GAA P CCA ස ප

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GAC
                                                                                                                                                s
TCA
                                                                                                                                                                                                                                                                                         N G K T G R G A V S E K D A P K E L
AAT GGT AAG GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
L S A K E G I D G R G G G H H H CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGG CAT CAT CAT
                                                                                                                                              M V K V K F K Y K G E E K E V D T
ATG GTG AAG GTTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT
                                                                                                                                                                                                                 K I K K V W R V G K M V S F T Y D AAG ATA AAG ATT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC
                                                                                                                                                                                                                                                                                                                                                                     *
TAG
                                                                                                                                                                                                                                                                                                                                                                   L D M L A R A E R E K K //
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //
                                                                        ::
                                                                         H H
CAT CAT
```

Figure 17PP

Pfu DNA Polymerase (WT) -Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 69) ccetggtect gggtecacat atatgttett actegeettt atgaagaate eeceagtege tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct aataccaatg gaggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaact tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga

aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag tagagocota tatocotoga ttataattao ocacaatgtt totooogata ototaaatot tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaagc gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt

aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt tttgctccaa gcagagccgc tccaatggat aacaccctg ttcccgcacc caagtccgct acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg aaagtataaat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctcttt taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa gtagaagcgg cactactcag atgettecee aggaatgagg ttgttgtage tentecenga aagattgaga tgttcttgg // // ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC AAT GGT AAG AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA

TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //TGA

Figure 17QQ

Sac7d - Pfu DNA Polymerase (WT) fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 61)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc ccccagtcgc totaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt aataccaatg gaggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct AAT GGT AAG ACA GGT AGA GCT GTA AGC GAG AAA GAT TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA AAA $^{\prime\prime}$

tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag cottocaatg gaaattcagc tttcaagatt agttggacaa cotttatggg atgtttcaag cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaact tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt tagagocota tatocotoga ttataattao ocacaatgtt totocogata ototaaatot tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaagc gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg

gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa aggogatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt

REPLACEMENT SHEET

FIGURE 1700 (CONT.)

ttccggggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa gtagaagcgg cactactcag atgetteece aggaatgagg ttgttgtage tenteeenga TGA aagattgaga tgttcttgg //

Figure 17RR

Sac7d - PFU DNA POLYMERASE (V93 R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 27) Nucleotide sequence (SEQ ID NO: 69) //Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

FIGURE 17RR (CONT.)

GAC GAC CCA AAA GAA TTA GAA GTA GAC ACT TIT ACC TAT GAT GCT TCC AAA GAG TGG AGA GTA GGC AAA ATG GTG GTA AGC GAG AAA GAA GGT AAG AAG TAT GGA GCT AGA TIC GGT AAG ATA AAG AAG GTT GTA AAG TTA GCA ACA GGT AAG AAG AAT

1020 1140 1380 1440 1500 1560 1680 1860 1080 1200 1260 1320 1740 1800 540 600 99 960 780 840 900 AAGGCATGGA CATTTACGCT AGAAAAGTT AAAGAGATAC TGGACAACCT ACTTAGGAAA GTGGGAAAAC GCTTGAATAT GCTATTCAAA CAAGCCTATT TCTTGCCTTC TATAATGATT TCTTCCATAC TATCAGGGAG ATATTTAGCG CGAGCCCAAG TTTCGACTTG AGCCTGGGAA GGCAACTTAT TCAAAGAAGG CAATGITICI AGTAGGCCAC GTTAGAGGAA AATACTCCTT TTATGGCTAT GGGAAGAAAG CCTCTACATT AAAGAAAAG AATAGATGAA TGAAATTGCA TGAAGAAGCT STGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG TGTATATGAA ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG TAACGGGGGA CCACTATTAG TTCCATTTGC GGGGAAGAAG AGCTAAAGAT TCGCATTCCC AGATAGCAAA TCGCTCCTCA TCTACGGATA GAGATTGGAG TTAGACCATA AAGGCCCAAT AAAACATAGA TTCTCAGGAT GAGATGGAAG GAAGAATACA CACTAGAGGC AAGATGCAAA AGTGGTTCTT AAGCCAAGTG AAGAGGAGTA TGGATTCGTT AAAGAGCCAG AAAAGGGGTT TAATTACCCA TTACTGCCTG GTGAGGAAAT GGTATGCAGT ACGGAGATGT AGTTTCTCGG CAAGATTAGT TGGGACATTT CTATAGAAAA GATTTAAAGT GACTGCTAGA GCA GAA AGA GAG AAG AAA GAGTTTGGAA AGTIGCCAAA TACTCGAIGG GATAGAGCAT GATAGAACTT GATTGAAGAA GTTAAGAAAA GGAACATCCC CAAGATXXXC GGACATCTTC GAATACGATA ATTACTTGGA GGAGACTCAT TACGCCGACG AACCTTGTAG CCCTCGATTA TGGTTTAGAG ATAGTTAGGA ATACTAAAAC GTTGAGAAAA GAGAGATG ATAAAGAGAT ACCATTGGAA GAAGTCAAGG CCAACATACA TCCAATGGAA ATTCAGCTTT AACTATGATA CCAAGTCTCT ACTCAAGATC GCAAATTCTT GCTGAGAGCG GAAAAGTTTG GGAGGAGAAA AAGCTCCCTG ATTCTTCGTT ACGAAGAAGA TGTAGAGAAG ACCAATGGAG CGAAGGAGAA AGCAAAGGTG GATTAAATTA GACGGCTGTA GGAGAAGGTA AAGCACAGGG AGCTCCAAAC AGCCCTATAT GGGATGCAAG TGGTTTTATA AAAACTCTTA CATAAATTCA TTTGGAGACA TACTTATAAT AATAAATCTC AATGAAGGAA TAAGGAGTGT GGAGCTCGAA AACTATCCCA AGA GAAAATTTAA ATGATTCAAA GAATTGTTGA AACTTTATT CAGCAGTTGT AAGGCCTAAT TATCAAGCGA AAAAACTTGG TAGGCGATAT TAACAAGGAC GAAAGCCAAA ACCTTGAGAG AAGAATTCCT TTTCAAGGTC GAAACGAAGT GCTACACAGG TAGATTTTAG TAAATCTTGA AAAAAGCGAT GATGGTACTG TAGTATGGAA GTCTCTATGC TTGTAAAATA ATAAGAGGGG TCATTACTCG CCCTCTATCA ATGAAAATGA ACATTATAGT AGGACATCCC TTAAGACAAA AAGCTAGAGT TTA GAC ATG AGTGGAGAGA AAGTTCTGCA GACTATAGAC ATGATTTAG AAAGAGAACG ACCGTGTGGA AGAGAACATC CTCATCGACA GATATAGAAA AGTTATGCAG AAGGATCCTG TATCATGTAA GAACTCGGGA TTATGGGATG CTCAGGGAGA ATAGTATACC AGACAAAAGA GACACTGATG GAAGGAAAAG CTTCTCAGGG AAGATTGTGA GTTGAGGTTG AAAAGGGCAG ATGCAGAGAA GCAATTTTTG GCCTACGAAA CCCGATACTC GCAAAAGCAA TACATCGAGT GCTCTAGAAT GAAGGGTTTT AAAGAAACTC

FIGURE 17RR (CONT.)

2100 2160 2220 2280 CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA AATGGTAATT GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC TAAAGCCAGG TTCCTGGCTT AACATTAAAA AATCC // GGAGTTAAAA AGCTGCTAAA GGATACATAG TACTTAGAGG TCGGCCTAAC CAAAGAAACT TACGATCCCA AAAAGCACAA GGATATTGGA ACAAGACAAG GCGGTACTTA GTAGCTGTTG // TGA

Figure 17SS

PPU DNA POLYMERASE (V93 R OR E) -Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) 540 909 9 CTGTTATTAG GCTATTCAAA TTAGACCATA CATTTACGCT TAACGGGGGA AAGGCATGGA AGAAAAAGTT TTCCATTTGC AAAGAGATAC TCTTGCCTTC TCTTCCATAC TTCTCAGGAT TATCAGGGAG TCGCATTCCC ATATTTAGCG CGAGCCCAAG TTTCGACTTG CACTAGAGGC TGTATATGAA AGATAGCAAA AGCCTGGGAA GGCAACTTAT TGGACAACCT TATAATGATT CAAGCCTATT GLUTAMIC ACID) CCACTATTAG GGGGAAGAAG AGCTAAAGAT AAGGCCCAAT AAAACATAGA GAGATGGAAG AAGATGCAAA CAAGATTAGT AGTTTCTCGG GAAGAATACA AGTIGCCAAA TACTCGAIGG V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT GTTAAGAAAA GAGTTTGGAA ATAAAGAGAT GGAGACTCAT TCCAATGGAA ATTCAGCTTT GTTGAGAAAA CAAGATXXXC GAATACGATA ATTACTTGGA ACCATTGGAA GAAGTCAAGG CCAACATACA TACGCCGACG GAGAGAGATG GATTGAAGAA TGTAGAGAAG GGACATCTTC ACCAATGGAG GATTAAATTA AATAAATCTC GGAACATCCC CGAAGGAGAA AGCAAAGGTG TACTTATAAT GACGGCTGTA GGAGAAGGTA AGTGGAGAGA ACCTTGAGAG ATGATTCAAA GAATTGTTGA CAGCAGTTGT AAGGCCTAAT ATGAAAATGA TAACAAGGAC SAACTCGGGA AAGAATTCCT AACTTTATT CCCTCTATCA TATCAAGCGA ACATTATAGT AAAAACTTGG TAGGCGATAT GAAAGCCAAA CTCATCGACA CTTCTCAGGG AGTTATGCAG AAGGATCCTG AAAAGGGCAG ATGCAGAGAA TATCATGTAA GCAATTTTG AAGATTGTGA ACCGTGTGGA AGAGAACATC GATATAGAAA GTTGAGGTTG

FIGURE 17SS (CONT.)

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1260
                                                       1320
                                                                     1380
                                                                                  1440
                                                                                                500
                                                                                                              1560
                                                                                                                           1620
                                                                                                                                         1680
                                                                                                                                                       1740
                                                                                                                                                                     1800
                                                                                                                                                                                  1860
                                                                                                                                                                                                1920
                                                                                                                                                                                                             1980
                                                                                                                                                                                                                           2040
                                                                                                                                                                                                                                         2100
                                                                                                                                                                                                                                                       2160
              1140
                                                       AGTAGGCCAC
                                                                   GTTAGAGGAA
                                                                                                                                                                                                            ACCAGAGAAG
                                                                                                                                                                                                                           AGGTCCTCAC
                                                                                                                                                                                                                                                       AGCTGAGGAA
                                                                                                                                                                                                                                                                    GGTTCTTCCA
ACTTAGGAAA
              TCAAAGAAGG
                            GTGGGAAAAC
                                          CAATGTTTCT
                                                                                  AATACTCCTT
                                                                                                TTATGGCTAT
                                                                                                              GGGAAGAAAG
                                                                                                                           CCTCTACATT
                                                                                                                                        AAAGAAAAG
                                                                                                                                                       GCTTGAATAT
                                                                                                                                                                     AATAGATGAA
                                                                                                                                                                                  TGAAATTGCA
                                                                                                                                                                                                TGAAGAAGCT
                                                                                                                                                                                                                                        AATGGTAATT
                                                                                                                                                                                                                                                                                 ATACCAAAAG
AACCTIGIAG AGIGGIICII
                                                                                                                                                                                 GAGATTGGAG
                                                                                                                                                                                                            ATGAAATTCC
                                                                                                                                                                                                                                        TAAAGCCAGG
                                                                                                                                                                                                                                                                  TGGAGAACCA
                                                                                                                                                                                                                                                                                GGGATTTGGA TACAGAAGG AAGACCTCAG
             AAGCCAAGTG AAGAGGAGTA
                                        TAATTACCCA
                                                       TCGCTCCTCA
                                                                   TGGGACATTT
                                                                                  CTATAGAAAA
                                                                                                TCTACGGATA
                                                                                                             TTACTGCCTG
                                                                                                                                        GTGAGGAAAT
                                                                                                                                                                   GGTATGCAGT
                                                                                                                                                                                               ACGGAGATGT
                                                                                                                                                                                                                          ATAAGGCGAT
                                                                                                                                                                                                                                                      GGGCAATTCT
                           AAAAGGGGTT
                                                                                                                           GATTTAAAGT
                                                                                                                                                      GACTGCTAGA
                                                                                                                                                                                                                                                                                             TTCCTGGCTT AACATTAAAA AATCC //
                                                                                                                                                                                                                                                     CGATGGTCCA ATTAGCAATA
                           AAAGAGCCAG
                                                       AACTATGATA
                                                                                                              GCTGAGAGCG
                                                                                                                           GAAAAGTTTG
                                                                                                                                        GGAGGAGAAA
                                                                                                                                                                                 ATAGTTAGGA
                                                                                                                                                                                                TITGGAGACA ATACTAAAAC
                                                                                                                                                                                                            CTTGCCAATT
                                                                                                                                                                                                                           TTACATGAGT
                                                                                                                                                                                                                                        AGCTGCTAAA GGAGTTAAAA
                                                                                                                                                                                                                                                                  GTATGACGCA GAATATTACA
                                          CCCTCGATTA
                                                                   CCAAGTCTCT
                                                                                  ACTCAAGATC
                                                                                                GCAAATTCTT
                                                                                                                                                      AAGCTCCCTG
                                                                                                                                                                    ACGAAGAAGA
AAGCACAGGG
                                                                                                                                                                                 TGGTTTAGAG
                                                                                  AATGAAGGAA
             AGCTCCAAAC
                                                       GGGATGCAAG
                                                                     TGGTTTTATA
                                                                                                                                        AACTATCCCA
                                                                                                                                                      CATAAATTCA
                                                                                                                                                                     ATTCTTCGTT
                                         AGCCCTATAT
                                                                                                AAAACTCTTA
                                                                                                                           GGAGCTCGAA
                                                                                                                                                                                                            AATACAAAAG
                                                                                                                                                                                                                          AACAAGACCA
                            TGGATTCGTT
                                                                                                              TAAGGAGTGT
                                                                                                                                                                                                                                                                                             ACAAGACAAG TCGGCCTAAC
                                                                                                                                                                                                                                       CAAAGAACT
TTTCAAGGTC
             GAAACGAAGT
                                        TAGATTTTAG
                                                       TAAATCTTGA
                                                                   AGGACATCCC
                                                                                  TTAAGACAAA
                                                                                                AAAAAGCGAT
                                                                                                                           TAGTATGGAA
                                                                                                                                        GTCTCTATGC
                                                                                                                                                                     ATAAGAGGG
                                                                                                                                                                                  TCATTACTCG
                                                                                                                                                                                                AAGCTAGAGT
                                                                                                                                                                                                            TAAAAGAAGT
                                                                                                                                                                                                                           ATGAGCAGAT
                                                                                                                                                                                                                                                      TACTTAGAGG
                                                                                                                                                                                                                                                                  AAAAGCACAA
                                                                                                                                                                                                                                                                                GGATATTGGA
                            GCTACACAGG
                                                                                                              GATGGTACTG
                                                                                                                                                       TTGTAAAATA
             GCCTACGAAA
                                                                                                                                                                   GAAGGGTTTT
                                                                                                                                                                                                                                                      GGATACATAG
                                                                                                                                                                                                                                                                  TACGATCCCA
TTATGGGATG
                           CTCAGGGAGA
                                        ATAGTATACC
                                                                                  AGACAAAAGA
                                                                                               GACTATAGAC
                                                                                                                                                                                GAAGGAAAAG
                                                                                                                                                                                                            GTGAGAATAG
                                                                                                                                                                                                                          CTCGCAATAT
                                                                                                                                                                                                                                       GTAGCTGTTG
                                                                                                                                                                                                                                                                                GCGGTACTTA
                                                       CCCGATACTC
                                                                     AAGTTCTGCA
                                                                                                              GCAAAAGCAA
                                                                                                                           TACATCGAGT
                                                                                                                                        GACACTGATG
                                                                                                                                                     GCTCTAGAAT
                                                                                                                                                                                                AAAGAAACTC
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CCA AAA GAA ACC TAT GAC GTA GAC ACT GAA TIT GCT GAG AAA ATG GTG TCC GAG AAA GAT GAA AGA GAG AAG AAA // GAA GTA GGC AAA TAT AAG GGT GCT GTA AGC GCA AAG AGA GGA TIC TGG AGA AGA ACA GGT GTA AAG AAG GTT ATG TTA GCA AAG AAG AAG AAG ATA GAC // ATG GTG AAT GGT

GAC

Figure 17TT

PFU DNA POLYMERASE (G387P/V93R OR E) -Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 69)

FIGURE 17TT (CONT.)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 1020 1140 1200 1260 1320 1380 1500 1560 1620 1680 1740 1800 1860 1920 1080 1440 540 840 900 or T) AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAG CACTAGAGGC TGTATATGAA AGTAGGCCAC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG TTAGACCATA CATTTACGCT CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT CGAGCCCAAG TTTCGACTTG GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA ACTTAGGAAA TCAAAGAAGG GTGGGAAAAC CAATGTTTCT GTTAGAGGAA GGGAAGAAAG CCTCTACATT GCTTGAATAT GAGATTGGAG TGAAATTGCA CTGTTATTAG GCTATTCAAA CAAGCCTATT AGAAAAGTT AAAGAGATAC TCTTGCCTTC TCTTCCATAC TATCAGGGAG ATATTTAGCG GGCAACTTAT TGGACAACCT AATACTCCTT TTATGGCTAT AATAGATGAA CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 3387P Mutant (CCN is the codon for Proline where N=C,G,A, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CCACTATTAG GGGGAAGAAG AGCTAAAGAT AAAACATAGA GAGAGATG ATAAAGAGAT TTCTCAGGAT GGAGACTCAT TCGCATTCCC GAGATGGAAG GAAGAATACA CAAGATTAGT TITCAAGGIC AAGCACAGGG AACCITGIAG AGIGGIICIT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA AACTATGATA TCGCTCCTCA TGGGACATTT CTATAGAAAA TCTACGGATA TTACTGCCTG GACTGCTAGA TTCCATTTGC AGTIGCCAAA TACTCGATGG AAGATGCAAA TAATTACCCA GAAAAGTTTG GATTTAAAGT GGTATGCAGT NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GCTGAGAGCG GAATACGATA AGCAAAGGTG ATTACTTGGA TGGTTTTATA CCAAGTCTCT V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC GAAAATTTAA GATAGAGCAT GATAGAACTT CAAGATXXXC ACCATTGGAA GAAGTCAAGG CCAACATACA TCCAATGGAA ATTCAGCTTT AGCCCTATAT CCCTCGATTA AATGAAGGAA ACTCAAGATC CATAAATTCA AAGCTCCCTG ACGAAGAAGA TGGTTTAGAG ATAGTTAGGA GCAAATTCTT GACGGCTGTA GGGATGCAAG AAAACTCTTA GGAACATCCC GGACATCTTC ACCAATGGAG TACTTATAAT GATTAAATTA AATAAATCTC TAAGGAGTGT GGAGCTCGAA ATTCTTCGTT TTAAGACAAA TAACAAGGAC GAATTGTTGA AACTTTATT CAGCAGTTGT CCCTCTATCA TATCAAGCGA ACATTATAGT AAAAACTTGG TAGGCGATAT GAAAGCCAAA ACCTTGAGAG AAGAATTCCT GAAACGAAGT GCTACACACC TAGATTTTAG AAGITCIGCA AGGACAICCC AAAAAGCGAT GATGGTACTG GTCTCTATGC TTGTAAAATA ATAAGAGGGG TCATTACTCG AAGGCCTAAT ATGAAAATGA TAAATCTTGA TAGTATGGAA CCCGATACTC AAAGAGAACG ATGCAGAGAA TTATGGGATG AGACAAAAGA GAAGGAAAAG AAAGAAACTC AAGATTGTGA ACCGTGTGGA GATATAGAAA AGTTATGCAG GTTGAGGTTG AAGGATCCTG AAAAGGGCAG TATCATGTAA AGTGGAGAGA GAACTCGGGA GCCTACGAAA CTCAGGGAGA ATAGTATACC GACTATAGAC GCAAAAGCAA TACATCGAGT GCTCTAGAAT SAAGGGTTTT AGAGAACATC CTCATCGACA GCAATTTTG GACACTGATG

FIGURE 17TT (CONT.)

2280 2160 CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT AGCTGAGGAA GGTTCTTCCA TACAGAAAGG AAGACCTCAG ATACCAAAAG CGATGGTCCA ATTAGCAATA GGGCAATTCT GAATATTACA TGGAGAACCA TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // GTATGACGCA GGGATTTGGA AAAAGCACAA GGATATTGGA TACTTAGAGG GGATACATAG TACGATCCCA ACAAGACAAG GTAGCTGTTG GCGGTACTTA

ACC TAT GAC GAC TTA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA GTA GAG AAA GAA GTG TCC TTT TGA GAA AGA GAG AAG AAA // ATG GAA GTA GGC AAA AGA GGA TTA GAC ATG TTA GCA AGA GCA AAG GTT TGG GGT AGA GTA AAG ACA AAT GGT AAG AAG ATA AAG ATG

:

Figure 17UU

PFU DNA POLYMERASE (G387P/V93R OR E) - Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG (ALL POSSIBLE CODONS FOR ARGININE) 300 G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T) CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT CTGTTATTAG GCTATTCAAA AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT CCACTATTAG AGAAAAGTT AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CAAGATXXXC ACCGIGIGGA AACTITATIT GGAACAICCC

FIGURE 17UU (CONT.)

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1080
                                                                                                                                                                                                                                                                     1380
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                                                                                                                                                                                                                                                                                                        1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                1920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2160
                                                                                                                                                            1020
                                                                                                                                                                                            GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
                                                                                                                                                                                                                                TAGATTITAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
                                                                                                                                                                                                                                                 GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
                                                                                                                                                                                                              GCTACACAGTTGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
                                                                                                                                                          CAAGATTAGT TGGACAACCT
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                                                                                                        CACTAGAGGC TGTATATGAA
                                                                                                                                         AGTIGCCAAA IACICGAIGG AAGAIGCAAA GGCAACIIAI
 TATAATGATT
                  AGCAAAGGIG ATTACTIGGA AAAACATAGA TCTICCATAC
                                   TATCAGGGAG
                                                    ATATTTAGCG
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                                                                                     GAAGAATACA TTTCGACTTG
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                                  GAGAGATG ATAAAGAGAT
                                                    GGAGACTCAT
                                                                                    GAAGTCAAGG
                                                                                                        CCAACATACA
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                                                                                    ATGCAGAGAA
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GAC GAC GTA GAC ACT CCA AAA GAA TAT ACC GCT GAA TTT TGA ICC GAG AAA GAT GAA AGA GAG AAG AAA // GAG GIG ATG GAA GCT GTA AGC GTA GGC AAA TAT AAG GGT GTA AAG TTC AAG AGA GGA GCA GCA AGA GIT IGG GGT AGA AAG ACA TTA AAG ATG ATG GTG AAG AAT GGT AAG TTA GAC AAG ATA >

E) fusion protein SAC7D-PFU DNA POLYMERASE (D141A/E143A/V93R OR

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 31) Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 32)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) G, A, or T) D141A/E143A Mutant (GCN is the codon for alanine where N = C, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

GAC ACC TAT GAC CCA AAA GAA GTA GAC ACT TTT GAA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TIC AAG TAT AAG GGT GAA GAG AAA TTA GCA AGA GCA GAA AGA GAG AAG AAA // // ATG GTG AAG GTA AAG AAT GGT AAG ACA TTA GAC ATG

1020 //ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 240 540 900 840 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 480 GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA GTTGAGAAAA AGTTTCTCGG CAAGCCTATT TTCCATTTGC AAAGAGATAC AAGGCCCAAT TATAATGATT TCTTCCATAC CGAGCCCAAG TTTCGACTTG TGTATATGAA AGCCTGGGAA TGGACAACCT AGTGGTTCTT ACTTAGGAAA AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG TCTTGCCTTC TATCAGGGAG ATATTAGCG CCACTATTAG AGAAAAGTT GGCAACTTAT CAAGATTAGT GGGGAAGAAG AGCTAAAGAT TTCTCAGGAT TCGCATTCCC GAGATGGAAG CACTAGAGGC AGATAGCAAA AAGATGCAAA AAAACATAGA GAAGAATACA GGACATCTTC GAATACGATA TTTCAAGGTC AAGCACAGGG AACCTTGTAG GAGTTTGGAA TACGCCGACG CAAGATXXXC ATTACTTGGA GAGAGATG ATAAAGAGAT GGAGACTCAT ACCATTGGAA GAAGTCAAGG CCAACATACA TACTCGATGG ATTCAGCTTT GGAACATCCC ACCAATGGAG CGAAGGAGAA AGCAAAGGTG GACGGCTGTA TGTAGAGAAG TACTTATAAT GATTAAATTA GGAGAAGGTA AGTTGCCAAA TCCAATGGAA AATAAATCTC AACTTTATTT ACCTTGAGAG SCCTACGAAA GAAACGAAGT ATGATTCAAA GAATTGTTGA CAGCAGTTGT AAGGCCTAAT CCCTCTATCA ATGAAAATGA TATCAAGCGA ACATTATAGT AAAAACTTGG TAGGCGATAT TAACAAGGAC GAAAGCCAAA AAGAATTCCT CTTCTCAGGG CTCATCGACA ACCGTGTGGA AGAGAACATC SAACTCGGGA LTATGGGATG AAGATTGTGA GCNATAGCNA AGTTATGCAG GTTGAGGTTG AAGGATCCTG AAAAGGGCAG ATGCAGAGAA **TATCATGTAA** GCAATTTTG AGTGGAGAGA

FIGURE 17VV (CONT.)

1560 1740 1800 1860 1920 2040 2100 2220 2280 TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260 AGTAGGCCAC 1320 1440 1620 1680 1980 2160 GCTACACAGTTGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 GTTAGAGGAA GGGAAGAAAG AAAGAAAAAG AATAGATGAA ATACTAAAAC ACGGAGATGT TGAAGAAGCT ACCAGAGAAG TTACATGAGT ATAAGGCGAT AGGTCCTCAC TACAGAAAGG AAGACCTCAG ATACCAAAAG TTATGGCTAT CCTCTACATT GCTTGAATAT AGCTGAGGAA GGTTCTTCCA CTATAGAAA AATACTCCTT TGAAATTGCA AATGGTAATT TCGCTCCTCA GTGAGGAAAT ATGAAATTCC GGGCAATTCT TGGGACATTT TCTACGGATA TTACTGCCTG GAAAAGTTTG GATTTAAAGT GAGATTGGAG GACTGCTAGA GGTATGCAGT TAAAGCCAGG TGGAGAACCA ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // CCAAGTCTCT CATAAATTCA AAGCTCCCTG CTTGCCAATT GGAGTTAAAA GAATATACA GGGATGCAAG AACTATGATA AATGAAGGAA ACTCAAGATC GCAAATTCTT GCTGAGAGCG GGAGGAGAAA ACGAAGAAGA ATAGTTAGGA ATTAGCAATA AAAACTCTTA ATTCTTCGTT GTATGACGCA TGGTTTTATA TAAGGAGTGT GGAGCTCGAA TGGTTTAGAG TTTGGAGACA AACAAGACCA AGCTGCTAAA GGGATTTGGA AACTATCCCA AATACAAAAG CGATGGTCCA AGGACATCCC TTAAGACAAA TAAATCTTGA AAAAAGCGAT TAGTATGGAA GTCTCTATGC TTGTAAAATA ATAAGAGGGG AAGCTAGAGT TAAAAGAAGT CTCGCAATAT ATGAGCAGAT CAAAGAAACT TACTTAGAGG AAAAGCACAA GGATATTGGA GATGGTACTG TCATTACTCG GACTATAGAC AAAGAAACTC GTGAGAATAG TACGATCCCA CTCAGGGAGA CCCGATACTC AAGTTCTGCA AGACAAAAGA GCAAAAGCAA TACATCGAGT GACACTGATG GCTCTAGAAT GAAGGGTTTT GAAGGAAAAG STAGCTGTTG GGATACATAG GCGCTACTTA ATAGTATACC

TGA

Figure 17WW

KOD DNA POLYMERASE - Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 69) 793R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) CTGTCATAAG AATTTTCAAG CAGCGATAAG GGACAAGATA TIGAACCCIA CIICIACGCC CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG GAGACCAGTT V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) AGTTCCTCGG GTTCAGAAGA ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC GATTGAGTAC GACCGGACTT GAGGICIGGA AACTCIACTT TACTCATCCG CAGGACXXXC CGGTTAAGCG GGTTGAAAAG AAGGAAAACG GCGAGTTTAA ACGGTTGTAA

FIGURE 17WW (CONT.)

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                                              TCTCCCCTAC
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              GGCGACGAGG AGCTGAAAAT
                              GAGTICGCCG AGGGGCCAAT
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TACCCTTCGC
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 TGACATCTAC
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                                                                                                                             PATCCTGTGA
                                                                                                                                            GCCGTCTTCG
                                                                                                                                                                            GAGCTTGGGA
                                                                                                                                                                                          CTCTGGGACG
                                                                                                                                                                                                          SCCTATGAGA
                                                                                                                                                                                                                                          GTGTACCTAG
                                                                                                                                                                                                                                                                                          CAGAAGATAA
                                                                                                                                                                                                                                                                                                         TACAGGCAGA
                                                                                                                                                                                                                                                                                                                         AGGCCCCCT
                                                                                                                                                                                                                                                                                                                                       ATAACGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                     GAGACGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACCCGACGA
```

Sac7d - kod dna polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 33) Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

1140 1020 //ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60 1080 540 900 840 AAGGAAAACG GCGAGITIAA GAITGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120 CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180 GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT CAGCGATAAG GGACAAGATA CCTTATGATA TACGCTGAGG AAATAACCAC AGCCTGGGAA CGGCCAGTCC TCACCCACAA CGTCTCGCCG CAAGCGCTAC GCTCGCCTTC TCTCCCCTAC TCCTCCGTGT TGTGAAGGAG CTATCTGAAA CGAGCCGAAG CTTCGATCTC CGTTTATGAA GGTCACATAC CCTCAGGAAG GGCCAGAAGA GGCGACGAGG AGCTGAAAAT TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT GGCCAGGGTG ATAACTTGGA AGAACGTGGA CGCTTGAGGC CTCGCTTAAT TACCCTTCGC TCGACTTCGC GGGATGGAAG GACGGATACA AAGATGCGAA CAGCACTGGC AACCTCGTTG AGTGGTTCCT GAGGGTTGTG GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GAGGGAGATG ATAAAGCGCT STGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TACTCATCCG CAGGACXXXC TGACATCTAC GAGTACGACA GGCGACAACT GCCCTCGGAA GTTTGCCGTC GAAGTGAAGG CCCACATACA TACTCGATGG TCCGATGGAG GCCCAGCTTT CTATGTAAAA GAGCCCGAGA AGTCGCCCGC GCCAATGGAA AACCTACAAC GGAGAAGGTT AATAAACTTC GATAAACCTG CICCIGAAGG ACGAIICIGC CGGTTAAGCG GAGGICIGGA AACTCTACTT CAGCAGTTAT AGGGATTAGT CTCTCTACCA ACGAGGAAGG TCTCGACGGA ACGTTCTCAT AAAAGCTCGG TGGGCGACAG TAAGACGGAC GTCAGCCGAA ACCTTGAGAG AGGAGTTCCT TCTCCCGCTC CGGCAGAGCT ATGAAGGAGG GGAATGAGCT GACATTGAAA GTTGACGTCG AAAGACCCGG ACCGGCGAGA GAGCTTGGGA CTCTGGGACG ACGGTTGTAA CTCATAGACA AGCTACGCCG ATTCAGAGGA TATCCTGTGA GCCTATGAGA CGAGAGCATC AAGCGCTGTG GCCGTCTTCG

FIGURE 17XX (CONT.)

1680 1740 1800 2040 2220 1440 1500 1560 1620 1860 1920 1980 2100 2160 1380 ITCIGCAAGG ACTICCCAGG AITIAICCCG AGCCTGCTIG GAGACCTCCT AGAGGAGAGG TTAAGGTAAT CTACAGCGAC GTGAGGCGTG ACTGGAGCGA GATAGCGAAA GTCAAAATAC GCCCTGGAAC GGTGATAAGC CGATACCGTT CGACGAGTTC CCCCACAGGT CGGCCACCGC TCGAGAGGAA GCTCCTCGAT CGGCTATGCA CGGCCTGGGG AAGGGAGTAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT CGAGTACGAG ATGCGGTGAT AGACGAGGAA TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG TCCCCACGTT AGACAGGITG GITIGAGIGC ITGGCIGAAG CCGAAGGGAA CI //TAG 2325 GAGGGATTTA AAGGACTACA AGGCAACCGG ACGGTTACTA CGCTTGAGCT AAGAAGAAGT SATACGCTCA ACAGAGGAAGG ATGCAAGGAA TATGACGTTG GAAGGCCACG ATTGACCCGA GATCCTGGCA AACAGCTACT GGAGTGTGCA GAGAGCGTAA GATAGAGGAA AAGTACGGCT CTTCCGGGCG GGCGACAGGG ACTTGAGATT CAACGCCAAA CTTCGTCACG TGGGAGGATA CGCGAGAGGA AGAAGAAGAT GGGCCATCAA TTTTGCCAC TCAAGTATAT AACGCGGCTT CAACGCGCGG CGAGGGTTCT AGAGGTTGGC TCAAGGGCTC GTTGAGAGAA TTCTGAGAGC GGTACTGCAA CCATCAAGGA AGGATAGTCA AAGAAGTTAC AGCAGATAAC GACCCGACGA AGCACAAGTA TACATCGTGC ACCGACGGAT STGATCCACG CAGAAGATAA AGGCCCCCT ATGGAGTTCC GGCTTCTACA GAGACGCAGG SCCGTTGCCA **TACAGGCAGA** ATAACGATGA GGCAAGATAA

Figure 17XY

Sac7d-Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 36) Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 35)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180 AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120 ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG

FIGURE 17YY (CONT.)

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1740
                                                                                                                                                                                1020
                                                                                                                                                                                              1080
                                                                                                                                                                                                           1140
                                                                                                                                                                                                                         1200
                                                                                                                                                                                                                                      1260
                                                                                                                                                                                                                                                   1320
                                                                                                                                                                                                                                                                 1380
                                                                                                                                                                                                                                                                                1440
                                                                                                                                                                                                                                                                                             1500
                                                                                                                                                                                                                                                                                                           1560
                                                                                                                                                                                                                                                                                                                        1620
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                                                                                                                                                                                                                                                                                                                                                                  1800
                                                                                                                                                                                                                                                                                                                                                                               1860
                                                                                                                                                                                                                                                                                                                                                                                             1920
                                                                                                                                                                                                                                                                                                                                                                                                          1980
                                                                                                                                                                                                                                                                                                                                                                                                                        2040
                                                                                                                                                                                                                                                                                                                                                                                                                                     2100
                                                                                                                                                    900
                                                                                                                                      840
                                                                                                                                                                  960
                                                                                               999
                                                                                                                                                                                             GTATCTTTTA
                                                                                                                                                                                                                                                   TCCGATAGTA
                                                                                                                                                                                                                                                                                                                                                                              AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTAAGGTAT
                                                                                                                                                                                                           AGAGTATAAA
                                                                                                                                                                                                                         AGGTTTGTGG
                                                                                                                                                                                                                                      TACTCACAAC
                                                                                                                                                                                                                                                                                                          CGCATGGGGG
                                                                                                                                                                                                                                                                                                                                      ACTCATTAAA
                                                                                                                                                                                                                                                                                                                                                                                             AAGTGTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                         GGTTCCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                        AGCCATTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCGGGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATTTTACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAACCAAGIT
             GGGCAAAATA
                           CAAGCGTTAT
                                         CCTTGCCTTT
                                                      AATAATGATT
                                                                    TTTGCCGTAT
                                                                                TGTTAAAGAA
                                                                                               GTATCTCATA
                                                                                                            ACATCCCGAA
                                                                                                                        AATCCACTTT
                                                                                                                                      TGAGGCAGTT
                                                                                                                                                    TGCCGCTATA
                                                                                                                                                                   TGCTAGGGCA
                                                                                                                                                                                 GCTGATAGGT
                                                                                                                                                                                                                                                                 GGACTTAATT
                                                                                                                                                                                                                                                                                CGAAAAGAAA
                                                                                                                                                                                                                                                                                             CGGCTATATG
                                                                                                                                                                                                                                                                                                                        TAAGGTTCTT
                                                                                                                                                                                                                                                                                                                                                   GCTTGAGCTT
                                                                                                                                                                                                                                                                                                                                                                  TGCAGTCATA
AAGGGAAGTT
                                                                                                                                                                                                                                                                                                                                                                                             GAGGCTATAC TTAAAGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                        AGGACTACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAAAGATAA GCGATAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAAGGAGGA
                                                     GAATTTGGAA AGGGCGAGAT
                                                                                                                                                    CAGAGGAAAT
                                                                                                                                                                  CAATGGAAGA
                                                                                                                                                                                AGCTGGCAAA
                                                                                                                                                                                                            CTGATGAGGA
                                                                                                                                                                                                                         AGCCAGAAAA
                                                                                                                                                                                                                                      CAATAATAGT
                                                                                                                                                                                                                                                   ACGATGTTGC
                                                                                                                                                                                                                                                                              TTGACCCGAT
                                                                                                                                                                                                                                                                                                          GAATGTGCTG AAAGCGTTAC
                                                                                                                                                                                                                                                                                                                        GATAAGAGAA ATAGAGGAAA AGTTCGGCTT
                                                                                                                                                                                                                                                                                                                                     TTATGCCACA ATACCCGGGG AAAAGCCTGA
                                                                                                                                                                                                                                                                                                                                                   TTCCAGGTCT
                                                                                                                                                                                                                                                                                                                                                                   AAAAGCGCTA
                                                                                                                                                                                                                                                                                                                                                                                                         CAAAATACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAAAGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTACATAGA
AATTTTGGG
                                       GGAGACGAGG AGCTTAAGCT
                                                                    AAAATATCGA
                                                                                 TTGTTCAAGT
                                                                                              TIGATITGCC
                                                                                                            GGGACAAAGA
                                                                                                                          TCAAGGGTAG
                                                                                                                                      CGTATACGCT
                                                                                                                                                                                              TCGTGGAGTG
                                                                                                                                                                                                                                                                 CCATACTCGG
                                                                                                                                                                                                                                                                                             ACAGCTATTA
              CAGCTATGCG
                          TACCCTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGCTCAAGA GGTAG 2325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATCCGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTGGATACA
                                                                     GGCCAGAGTA ATCACATGGA
                                                                                                                                                                                                                                                                                                                                                                  TTTGTTACAA
                                                                                                                                                                                                                                                                                                                                                                                                                        AGGGATTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAAGAGGGA
                                                                                                                                                                                                                                      CTGTACCCTT
                                                                                                                                                                                                                                                                                                                                                                                                          GAGAAAATAG
                          GAATATGACA
                                                                                               GGGGACAATT
                                                                                                                         GCTGTGGAAA
                                                                                                                                      AAGGACGATA AACCTCCCAA
                                                                                                                                                                   GCCCAGTACT
                                                                                                                                                                                 ATGGAAGCTG
                                                                                                                                                                                              GAGATCAAGC ACCGGCAACC
                                                                                                                                                                                                                                                    TGTAAGAATT
                                                                                                                                                                                                                                                                               AAATCCACAA
                                                                                                                                                                                                                                                                                             TTGCTTGCAA
                                                                                                                                                                                                                                                                                                                                                   AAACTACATA AACTCCAAAC
GTCAGGAAAA
              CAAGACXXXC
                                                                                AAGAGAATG ATAAAGCGTT
                                                                                                             GTCTTAGGAA
                                                                                                                                                     AAATTAGGAG
                                                                                                                                                                                                            CCGAACAAAC
                                                                                                                                                                                                                         TATGTAAAAG
                                                                                                                                                                                                                                                                  TTTATTCCCT
                                                                                                                                                                                                                                                    AAAAGAGGC
                                                                                                                                                                                                                                                                                                           GTACTCGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTAGATGCA
                                                                                                                                                                                                                                                                  CTTTCCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                          AGATGTTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGATTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAAGGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACACAAGTAC
                                                                                                                                                                                ATTCTTCCCC
                                                                                                                                                                                                            TGAACTTGCA
                                                                                                                                                                                                                                      TTTCCGCAGT
                                                                                                                                                                                                                                                                               GAAGAAAATG
                                                                                                                                                                                                                                                                                             GGCTATTAAA
                                                                                                                                                                                                                                                                                                                                                                  GAGAGGATTC
                                                                                                                                                                                                                                                                                                                                                                                              AAAGGTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGACTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTCGAAGCG
                                                     TGAGGGAGAT
                                                                                               AACTTACAAT
                                                                                                                          TGATAGTTTT
                                                                                                                                                     AACCAAAAGC
                                                                                                                                                                   GAAAAAACTA
                                                                                                                                                                                                                         CCTGGGAGGA
TGCAGTGAAA
              CGAGCATCCC
                           TGACATTTAC
                                         TCCCATGGAG
                                                                                                              AGTTCGGCTT
                                                                                                                                                                                                                                                                                                                                       CTGACGGCTT
                                                                                                                                                                                                                                                                                                                                                                               GCAGGATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACAAACCGG
                                                                                                                                        CAGTTGTGCG
                                                                                                                                                                                              GGGACGTCTC
                                                                                                                                                                                                            ACGCGAGGAA
                                                                                                                                                                                                                                                                  TCTGCAAGGA
                                                                                                                                                                                                                                                                                                                                                    AGGAATTCCT
                                                                                                                                                                                                                                                                                                                                                                  GCTTTTACTT
                                                                                                                                                                                                                                                                                                                                                                                               AGACTCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                           AAGTTGTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                        TTATCCATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCCTAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACTTAGGAT
                                                                                                                                                      TTTTAGGAAA
                                                                                                                                                                                                                                        TTTATTTGGA
                                                                                                                                                                                                                                                     ATACCCTTGA
                                                                                                                                                                                                                                                                               AAGATATAAA
                                                                                                                                                                                                                                                                                                           AGGCAAGATG
                                                                                                                                                                                                                                                                                                                        TAGAGATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                       CGATAGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATATCGTTCT
 GAGTGCTCGA
                                                       CGTTTTATCA
                                                                      ATGAAGAAGA
                                                                                  TGTCCAATGA
                                                                                               ATGTGATAAT
                                                                                                             AAAAGCTGGG
                                                                                                                          AGAGGATGGG
                                                                                                                                                                   AAGAAAGCAT
                                                                                                                                                                                  TCGGGAAGGA
                                                                                                                                                                                                                         GAACAACTTA
                                                                                                                                                                                                                                                                                             ATAGGCAAAG
               AGCTCATTTT
                           CAGCTGTGGT
                                          AGGGCTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATAATAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAAGCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                          AAAGCTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGCCGGCAG
                                                                                                                                                                                              CAAAGTGTAT
                                                                                                                                                                                                                                                                                                                                        TATGCGGACA
                                                                                                                                                                                                                                                                                                                                                    AAGAAAGCCA
                                                                                                                                                                                                                                                                                                                                                                                             ATAGCTAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCATGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGAATACG
               GAAGTCTGGA
                                                      GATATTGAAA
                                                                                               AAAGACCCCG
                                                                                                                          CCCAAGATTC
                                                                                                                                                       TATGAAGCAG
                                                                                                                                                                   TGGGAAACAG
                                                                                                                                                                                                                                        GAAAATATCA
                                                                                                                                                                                                                                                    GTATCCCCAG
                                                                                                                                                                                                                                                                               GCAATGAGGC
                                                                                                                                                                                                                                                                                             ATGCTCGATT
                                                                                                                                                                                                                                                                                                                        AGACACTACA
                                                                                                                                                                                                                                                                                                                                                                  GAGTATGAGG
                                                                                                                                                                                                                                                                                                                                                                               GATGAAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                          GAAAAGCTTG
  AAAACTGTGA
                           AGGGAACATC
                                         CTCATAGACA
                                                                     AGTTATGCCG
                                                                                   GTCGATGTTG
                                                                                                              AAACGGGCAG
                                                                                                                                        GATCTTTTCC
                                                                                                                                                                                 ACGTATGAGC
                                                                                                                                                                                                             AGGGTGGCAT
                                                                                                                                                                                                                           CGGCGCTTAA
                                                                                                                                                                                                                                                                  GGATATAGGT
                                                                                                                                                                                                                                                                                                             GGGTATCCTA
```

Figure 17ZZ

Vent DNA POLYMERASE - Sac7d FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 35)

CGT (ALL POSSIBLE CODONS FOR ARGININE) = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) cgg, gga, CGA, AGG, = AGA, V93E MUTANT: XXX V93R MUTANT: XXX

1200 1380 1020 1080 1140 840 900 99 900 TGTTAAAGAA GGGCAAAATA GTATCTCATA TGCCGCTATA AGAGTATAAA TACTCACAAC CTATAATCCG AATTTTAAG TATATATGCT GAGACATGGA AAGGGAAGTT CAAGCGTTAT CCTIGCCTIT AATAATGATT TTTGCCGTAT ACATCCCGAA AATCCACTTT TGAGGCAGTT TGCTAGGGCA GCTGATAGGT GTATCTTTA AGGTTTGTGG TCCGATAGTA GGACTTAATT TTCAGCCCTA TAAAGGGCGA AGGCCGAGAT GGGACAAAGA TCAAGGGTAG CGTATACGCT TCGTGGAGTG ACGATGTTGC CCATACTCGG AATTTTGGG CAGCTATGCG TACCCTTTGC TTGTTCAAGT TTGATTTGCC CAGAGGAAAT CAATGGAAGA AGCTGGCAAA CTGATGAGGA AGCCAGAAAA CAATAATAGT AGCTTAAGCT AAAATATCGA TGAGGGAGAT GAATTTGGAA CATAACAAAA GATGGCAAGC ATAAAGGCAA GTCAGGAAAA GAATATGACA GGAGACGAGG ATCACATGGA AAGAGAATG ATAAAGCGTT AACCAAAAGC AAATTAGGAG CTTTCCGGGC TTTATTCCCT GACCCTCATT CGAGCATCCC CAAGACXXXC GGGGACAATT GTCTTAGGAA GCTGTGGAAA AACCTCCCAA GCCCAGTACT ATGGAAGCTG ACCGGCAACC CCGAACAAAC TATGTAAAAG CTGTACCCTT TGTAAGAATT AAGGACGATA TATTGAGGAG TGACATTTAC GGCCAGAGTA GAAAAAACTA GAGATCAAGC CCTGGGAGGA TCCCATGGAG AACTTACAAT TGATAGTTTT ATTCTTCCCC TTTCCGCAGT AAAAGAGGGC AATAGAACTT TGCAGTGAAA AGTTCGGCTT TGAACTTGCA TGTCCAATGA CAGTTGTGCG AGAGGATGGG TTTTAGGAAA ATGACTCCGC ATGTGATAAT AAGAAAGCAT ACACTGATTA GGGAGTTTAA GAGTGCTCGA AGCTCATTT CAGCTGTGGT AGGGCTTGAT CGTTTTATCA AAAAGCTGGG TCGGGAAGGA GGGACGTCTC ACGCGAGGAA GAACAACTTA TTTATTGGA ATACCCTTGA TCTGCAAGGA ATGAAGAAGA GGATATAGGT ATGATACTGG CTTCTCAAAG GAAGTCTGGA CTCATAGACA GATATTGAAA AGTTATGCCG AAAGACCCCG AAACGGGCAG CCCAAGATTC GATCTTTCC TATGAAGCAG TGGGAAACAG CAAAGTGTAT AAAGAGAACG AAAACTGTGA AGGGAACATC GTCGATGTTG ACGTATGAGC AGGGTGGCAT CGGCGCTTAA GAAAATATCA GTATCCCCAG

FIGURE 17ZZ (CONT.)

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1560
                                                     1620
                                                                      1680
                                                                                        1740
                                                                                                            1800
                                                                                                                               1860
                                                                                                                                                1920
                                                                                                                                                                   1980
                                                                                                                                                                                     2040
                                                                                                                                                                                                       2100
                                                                                                                                                                                                                           2160
                                                                                                                                                                                                                         AATTTTACTT
                                                                       CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA
                                                                                                                                                AAGTGTTGAA
                                                                                                                                                                                                      ACCGGGCACA
                                                    TAAGGTTCTT
                                                                                        GCTTGAGCTT
                                                                                                            TGCAGTCATA
                                                                                                                              TTGGAGTGAG
                                                                                                                                                                                     AGCCATTGGC
                                                                                                                                                                                                                                              AAACCAAGTT
                                                                                                                                                                                                                                                               TTTAAGGTAT
CGAAAAGAAA
               CGGCTATATG
                                   CGCATGGGGG
                                                                                                                                                                   GGTTCCACTT
                                                                                                                                                                                                                                            ACACAAGTAC GATCCGGACT ACTACATAGA
                                                                                                                                                                                                                                                               ITGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA
                                                                                                                                                                                     AGGACTACAA
               ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA
                                                    GATAAGAGA ATAGAGGAAA AGTTCGGCTT
                                                                                                             TTTGTTACAA AAAAGCGCTA
                                                                                                                               AACAAGGGG TTGGAAGTAG TAAGGAGAGA
                                                                                                                                                AAAGGTTTTA GAGGCTATAC TTAAAGAGGG
                                                                                                                                                                 AGATGTTGTA GAGAAAATAG CAAAATACAG
                                                                                                                                                                                                       TAAAAGTGAA
                                                                                                                                                                                                                         CAAAGGGAGC GGAAAGATAA GCGATAGGGT
SCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT
                                  GTACTCGAAG GAATGTGCTG AAAGCGTTAC
                                                                                        AAACTACATA AACTCCAAAC TTCCAGGTCT
                                                                                                                                                                                                                                                                                CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //
                                                                                                                                                                                     GCAGATTACC AGGGATTTAA
                                                                                                                                                                                                       AAGACTTGCC GCAAGAGGGA
                                                                                                             GAGAGGATTC
                                  AGGCAAGATG
                                                                                           AGGAATTCCT
                                                                                                                                                                    AAGTTGTTAG
                                                                                                                                                                                     TTATCCATGA
                                                                                                                                                                                                                                              ATCCTAGAAA
                                                     TAGAGATGAC
                                                                                                                                                AGACTCAGGC
                                                                                                                                                                                                       CGATAGCAAA
                                                                                                                                                                                                                         ATATCGTTCT
                                                                                                                               GCAGGATAAC
                                                                                                              GCTTTTACTT
                                                                                                                                                                   AAAGCTGTAG
                                                                                                                                                                                                                        ATAATAAGCT
                                                                                                                                                                                                                                             ACAGAATACG
               ATGCTCGATT
                                   GGGTATCCTA
                                                                                                                                                ATAGCTAAGG
                                                                                                                                                                                     GAAAAGCTTG
                                                      AGACACTACA
                                                                         TATGCGGACA
                                                                                            AAGAAAGCCA
                                                                                                             GAGTATGAGG
                                                                                                                               GATGAAGAGG
                                                                                                                                                                                                       CCTCATGTCG
```

GAC TTT ACC TAT GAC GCT CCA AAA GAA GAA GTA GAC ACT TGA TGG AGA GTA GGC AAA ATG GTG TCC GAA GAG AAA GGA GCT GTA AGC GAG AAA GAT TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // GGT AAG TAT AAG TIC AAT GGT AAG ACA GGT AGA AAG ATA AAG AAG GTT GTA AAG AAG // ATG GTG

Figure 17AAA

Deep Vent- Sac7d DNA polymerase fusion protein

// Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 38)

FIGURE 17AAA (CONI.)

S FOR ARGININE) 60 120 120 300 300 420 660 720 780 840 900 1020 1140 11380	1440 1500 1560 1620 1740 1860 1920 1980 2100
O (1)	GAAGATGCTT TTATGGGTAC GGGGAGGGAA CTTATACATA AAAGAAAA GCTTGAGTAC GATAGATGAG CGAAATAGCC TGAGAAAAAG TCCAGAAAAAG AGGTCCGCAC AGGTCCGCAC CATGGTGATA
CGT (ALL GLUTAMIC CGAȚTATAA TTAGACCTI TAACCGCCG AGTTCCTGG AGTTCCTCAGG AGACGGTCAAGI AGGGGCCCAA AAAAGATCG CCCTCCAAGG CCCTCCAAGG AGAAAGGGC AGGATGCTAG AGAAAGGGC AGAAAAGGGC TCGCCCAGG AGAAAGGGC TCGCCCCCC AGAAAAGGGC TCGCCCCCCCCC AGAAAAGGGC TCGCCCCAGG TCGCCCCAGG AGAAAAGGGC TCGCCCCAGG TCGCCCAGG TCGCCCCAGG TCGCCCCAGG TCGCCCCAGG TCGCCCCAGG TCGCCCCAGG TCGCCCCAGG TCGCCCCAGG TCCCCCAGG TCCCCCCAGG TCCCCCCCAGG TCCCCCCCCCC	CAATCGAGAA ATTATGGTA TTACGGCCTG GGTTCAAAGT CCGAGGAGAT GGCTGTTGGA AGTATGCGT AGGACTGGAG ATGGCAACGT ACGAAATACC ACGAAATACC ACGACACCT ACGAAATACC ACGACACCT ACGACACCT ACGACACCT ACGACCT ACGACCT ACGACCT ACGACCT ACGACCT ACGACCT ACGACCT ACGACCT ACGACCT ACGCCT ACCCT ACGCCT ACGC
	TCTAAAGACC GCAAACAGCT GCAGAGAGCG GAAAAGTTCG GGGGCAAAAC AAGCTCCCAG ACGAAGAAGA ATAGTCAGGA ATCCTAAAGC CTGAGCAAGT CTTCACGAGT GGAGTAAAGG
A, AGG, CGA, CATCACCGAG GGTTGAGTAC GATTGATGAG TGCCGAAAAG TGCCAATGTT TCCAATGGAA CGAAGGGAG AGCCAAAGT TACCTACACC GATAAAGCT GAGGAGATG TACCTACAC GAGGAAAGT TACCTACAAC GAGGAAAGT TACCTACAAC GAGGAAAGT AGTTGCAAAG GCCCCAATGGAG TTCCAATGGAG TTCCAATGGAG GGGATACTT AGTTGCAAAG TTCCAATGGAG GGGGTTATATC AGGGTTATATC	GATGAAAGCT CAAAATCCTG TAAGGAGTGC GGAACTGGAG CACAATTCCT TATAAACGCC GTTCTTCGTG GGGCTTGAA CCTAGAGGCT AACTGAAAAG CACGAGGCCC AGCCGCTAGA
	TAAAAAGGAA AACGGCCAAT GTTGGTAAGGAA GACTCTAAGGAA TCGTAAGAATTA ACGTGAGAGG TAATCACTAG AAGCAAAAGGT TTAAGGAGGT TTAAGGAGGT TCAAAAAGGTT
V93R MUTANT: V93E MUTANT: ATGATACTTG AAAGAAACG G CTCCTCAAAG AAGATAGTGA G GAGGTATGGA G AGAGTATGGA AGACTATGCTG AAGACTACTG AAGATCCCG AAGACGCCG AAGACGCCG AAGACGCCG AAGACGCCG AAGACGCGCG AAGACGCGCG AAGACGCGCG AAGACGCGCG AAGCCCGCGTA G CTGTGGGAAAGG G ACTGGAAAGG G ACTGGAAAGG G ACTGGAAAGG G ACTGGAAAGG G CTGTGGGATG T CCCGGATACCC T AAGTTTCCC T AAGTTTCCC T	AGGCAAGAAA GATTACAGGC GCAAAAGCCC TATATAGAGT GACACAGATG GCCCTAGAGT GAGGGCTTCT GAAGGAAGC GTAAAAACCC GTAAAAAACCC GTAAAGATAG CTAGTTATTT GTTGCCGTGG

FIGURE 17AAA (CONT.)

GCC	GATC GTTC AAAC	TCA	GGA1 GAA1 CAGC	AGCAT FATT?	raa c	STATC SGCCT SGCAT	3ACGC FTTGC FGGCT	11 G1 E1	TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATC GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCA ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG //	TACA	AAG	AAAA ACCI	TCAG CAG	TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG ACTAAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG //	TTAC	AG	2220 2280 2328	
>	ATG AAG AAT	GTG ATA GGT	AAG AAG AAG	GTA AAG ACA	AAG GTT GGT	TTC TGG AGA	AAG AGA GGA	TAT GTA GCT	ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAA AAA AAG ATA AAG ATT TGG AGA GTA GGC AAA ATG GTG TCC TTT AAT GGT AAG AGA GGA GCT GTA AGC GAG AAA GAT GCT TTA GAC ATG TTA GCA AGA GCA GAA AGA AGA AAA AAA AAA AA	GGT AAA AGC GAG	GAA ATG GAG	GAG GTG AAA	AAA TCC GAT	// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC AAT GGT AAG ACA GGT AGA GCA GTA AGG GAG AAA GAA GAA GAA TTA TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA AAA AA	GTA ACC CCA	gac tat aaa	ACT GAC GAA	TCA GAC TTA

Figure 17BBB

Sac7d - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 38) Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 37)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC AAT GGT AAG ACA GGT AGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

9 240 300 360 420 480 540 600 99 840 006 1020 1080 720 780 960 1140 1200 1260 1320 //ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC GATAAGGGAG CGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT GGATAAGATA GAAGAGGTAC TGAGCCAAAG AGTTTATGAG GGCCTGGGAG GGTAACGTAC CCTCAGGAAG CGAGAGAAGG GCTCGCALTI GAAGGATACA CTTTGACCTC CGGCCAGCCC CTATCTAGTI CCGCAATAAG TTCCGTTCGC AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GGGACGGTAG CCCTCGAGGC AGGATGCAAA CAAGGTTAGT TICAACIGGC AACTIGGIGG AGIGGIACCI GGCTCCAAAC AAGCCGGATG AGAGGGAGTA TAATCACCCA TCCTCAAGGT TCGACCTTCC AGATAGCTGA AGAAAGGGCT CAGGACXXXC AGTIGCAAAG TATICAAIGG GAGTACGACA GAGGGAGATG ATAAAGCGGT GGCGATTCTT CCCCTGGGAA CCAACATACA TACGCTCACG CCCAATGGAG GCCCAGCTTT GGGATACGTT AAGGAGCCGG GAGCCTGTAC CCCTCGATAA GACAGCGGTG GAGATAAAGG TGAACACCCT CCGCAGTIAT TGACATCTIT TACCTACAAC GATAAAGCTA GATAAACCTC GGAGAAAGTT GGCTGTACTT TAGATTTCAG ATGACTCGCA CCCTCTATCA ATGAGGAAGA TTTCCAGCGA ATGTTATAAT AAAAGCTCGG TTGGGGGATAT TTAGGAGAAC GAAAGCCAAA GACTGGAGAG GGGAGTTCTT TTTCTAGGTC GCTACGCTGG GGAATGAATT CTCCTCAAAG CTAATAGACA AGCTATGCTG AAGAGGGCCG TAGTTTCCC GTCGAGGTAG AAAGATCCCG ATGCAGAGGC TACCACGTGA GCAATCTTCG ACTGGAAAGG CTGTGGGATG GCCTACGAGA CTAAGGGAGA GAGGTATGGA AGAGAGCATT GACATAGAAA GAGCTCGGTA

REPLACEMENT SHEET

FIGURE 17BBB (CONT.)

AAGTTCTGCA	AAGTICIGCA AGGACTICCC GGGGITITAIC CCCAGCCIGC ICAAGAGGIT AIIGGAIGAA	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	TAAAAAGGAA GATGAAAGCT	TCTAAAGACC	CAATCGAGAA GAAGATGCTT	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAACTGGAG	GAAAAGTTCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC		CACAATTCCT GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA		TATAAACGCC AAGCTCCCAG	GGCTGTTGGA GCTTGAGTAC	GCTTGAGTAC	1740
GAGGCTTCT	ACGTGAGAGG		ACGAAGAAGA	GITCITCGIG ACGAAGAAGA AGIAIGCGII	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGCCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAAGATAG		TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GTATGACGCT GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220
GCCGTTCTTA		GAATATTAGA GGCCTTTGGG	TACAGGAAAG	TACAGGAAAG AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17CCC

JDF-3 - Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAGGCTTAAACTCATGTCCTTCGACATCGACACCTCTACCACGAGGGGAGAAGAGTTTGGAA GGGGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGGGCGCGGAGAAGGTGAAGAAAAAGTTCCTCGG CAGGICTGIGGAGGICTIGGGICCTTIACTICACGCACCCGCAGGACXXXCCGGCAAICCGCGACAAAIAAGGAAGCACCCCGCGGGICAICGACAICIACGAGIACGACAIACCC GCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCCGGACGTGCTGATAACATACGACGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTTGGCGTGAGCTTT ACCCTCGGGAGGGACGGGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATAAGGCCCATAAA ACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCCGGCGAGGGGGCTTGAGAG ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCTTACTACTTCT

FIGURE 17CCC (CONT.)

acgecegregetaceteaaggagecegagegggactgregggacaatategretatetagactttcgtagtetetad<mark>ect</mark>freaateateateaeeeaeetetegeeagatae SAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCGCGGGCTTGAGATAGTCAGGCGC CGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCCG CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAATCTCCTTCGATTACAGGCAACGGGGGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT **ATGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGGTTGAGGAAAAGTTCGGTTTTAAAGTCCT** ACTGGAGCGAGATAGCGAAGGAGGCGAGGCGAGGGTTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAAATTGTCAGGGAAGTCACCGAAAAAGCTGAGCAA GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACGGCCCGCACGTAGCCATAGCGAAgcGTTTGGCCGCAGAGGT 3GTCGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCC GTGGCTGAAGCCGAAGGGGAAGAAGAAG//

Figure 17DDD

Sac7d - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 40) Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 39)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

AAT GGT AAG ACA GGT AGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC // ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

FIGURE 17DDD (CONT.)

CCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCCTTCGAAATCGAAACACTCTTCGAAACAAGAGAAGAAGTTTGG CTACGCCGGTGGCTACGTCAAGGAGCCGGAGCGGGGACTGTGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTAACCTTTCAATCATAATCACCCACACGTCTCGCCAGAT **GGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAATCTCCTCGATTACAGGCAACGGCGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGG** TCGAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCGCGGGCTTGAGATAGTCAGGCG TGCGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGC CTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGGAGAAGGTGAAAAAAGTTCCTC GGCAGGTCTGTGGAGGTCTTGGGTCCTTCACGCACCCGCAGGACXXXCCGGCAATCCGCGACAAATAAGGAAGCACCCCGCGGTCATCGACATCTACGAGTACGACATAAC TTACCCTCGGGAGGGACGGGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACCAT AAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGGCCCAAGGAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGGCTTGAG AGGGTCGCGCCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTT ACGCTCAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCCCGAGGTCACAAGTTCTGCAAGGACTTCCCGGGCTTCATTCCGAGCCTGCTCGAAACCTGCTGGAGGAAA CTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGGGGGGCGTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATAAATCCCAAACTGCCGGGCCTTC aagcgcttcttgagggtcgttaaggaggaaggacgtgatgataacatacgacgacgacaacttcgactacctgaaaaaagcgctgtgagaagcttggcgtgagcgt //ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCTACTT SCGTGGCTGAAGCCGAAGGGGAAGAAGAAGTGA

Figure 17EEE

Synthetic Sso7d gene:

Nucleotide sequence (SEQ ID NO: 71) Amino acid sequence (SEQ ID NO: 72) A T V K F K Y K G E E K E V D I S K GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG I K K V W R V G K M I S F T Y D E G ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAG GGC G G K T G R G A V S E K D A P K E L GGT GGC AAG AC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CGG AAG GAG CTG L Q M L E K Q K K CTG CAG ATG CTG GAG AAG AAG

Figure 17FFF

Sso7d-Taq DNA polymerase fusion protein

Amino acid sequence (SEQ ID NO: 72) // Amino acid sequence (SEQ ID NO: 66) Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 65)

```
// A T V K F K Y K G E E K E V D I S K
                                                                                                             I K K V W R V G K M I S F T Y D E G ATC ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
                                                                                                                                                                                                                         G G K T G R G A V S E K D A P K E L GGT GGT GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
                                                                                                                                                                                                                                                                                                                                         L Q M L E K Q K K //
CTG CAG ATG CTG GAG AAG AAG //
```

V GTG ACC K AAG PCCA ი წმ Y d b r AAA ¥ TGG K AAG GAA GIG CIG ACC L 4 D T ACG T. CTG AGC DGAC ი წმ CAG V GTC L I ຜ GCC CCC gcc Gcc CIC CIC CTC K AAG r CTC A GCC E GAC စ ဗ္ဗ s AGC K AAG V GTC ဗ္ဗဗ္ဗ s AGC **A** A GCC DGAC T ACC E GAG CTG က် က ကို ည မှ ည g GGG ළ ශීශී K AAG V GTC CTC CGG K AAG GAC V GTG CAC CAC R AGG r CTT ¥ FGG ය විවි ရင္ပင CŢĠ acc acc F ဝ ဝင္ပင r GTG DGAC IATC Gic r CTG N AAC E I ATC GGC 7 K AAG GCC GCC A GCG E GAG DGAC v GTC D GAC E F V GTC ရင္ပင A GCC Ы K AAG K AAG CAC g gc A GCG V GTC GGC CGC V GTG CAC Y S TCC ပိုင္ပင္ပ r G Ω Y F I ATC E GAG E GAG IATC E Y TAC I ATC K AAG E K AAG r CTT Z ი გმ CIC Y TAC Y V GTC CGC T ACC V GTG GAA GAC F TTT K AAG r G S ი მმ gcc Gcc r CHO အင္လ A GCG A GCG ය ශීශී් ဗဗ္ဗ D GAC W ය ශීශීශී R AGG යියිය Н GGG Y TAC CAG D Y TAC r Ci ල් වි S E CTT T ACC A GCG DGAC × GCC GCC V GTG ი მმც A GCC CAA CAA V GTC K AAG LCTT r CTG ₩ TGG L CTG T ACG CIG J M ATG r CTG P CCG DGAC E GAG ය උදි E GAA CIC GCC ₽ 900 K AAG N AAC Ω ი ცვ CAC GAG CAC A GCG E က ည CIC o CAG ය ද්ර CGG K AAG EGAG Д S AGT CAC g GGG සි F TTT င္ပင္ပင္သ K AAG Y A A G ACC Y CTC ი მმ Σ ACT ဗ္ဗဋ္ဌ සි පි F TTC DGAC ₽ GCG K AAG Ciri D GAC r CFC IATC IATC Gr H . GCC -V GTC D 3AC န နှင့်င D GAC A GCC S E r CTG L gg A ၁၉ A GC GC

A **₽** A GCC စ ဗ္ဗ F R GGG V GTG IATC L GT 3 3 3 3 r CTG L CTG K AAA V GTT r CHC r CTC Y TAC ი მემ R R G G ဗ ဗ္ဗ ව පිරි Y EGAG ч Б CGC R AGG L T ACG CIC F TTC E L CTT Y TAT s AGC ස් වි EGAG AAC AAC GTG E ස වි GAG P DGAT PCCT CTG M ATG R GG ¥ N A GCC 4 S F AAG r CTT DGAC A GCC E GAG GAC CCC **₽** S TCC E CAC မှ ငြင် V GTG D GAC V GTG CTT ggg မှ ည CHC က် ကို W CCC A AA r CTC M ATG GAG CAC A GCC CIG CIC W TGG M ATG A GCC gcc D GAC ი მვვ R AGG CAC r CTG ဗဗ္ဗ E GAC ဗ္ဗဋ္ဌ E ₽ GCC န TCC S AGC CCC က် ည cgg Sgg r CHC E A GCC gc A ස පු TGG ဗ္ဗဗ္ဗ A GCC E GAG H CIT GCC CCC ကို ည GG R EGAG CIG R AGG L ITG CIG TCC E GAG K AAG T ACC E უ წე v GTC F V GTC ပ ညီ P CCG မှ ည အင္တ A A A ACC ი მვ E GGG R AAG CTC GCC GAG GGC ස දිපි CIC GCT R AGG F EGAG N AAC F ဗ္ဗဋ္ဌ A GCG CTT CIG S TCC g GGC A GCG 급 TCC r CTC V GTC Ø E GAG (CTG s TCC GCC EGAG L R AGG CIT Y TAT E D GAC R AGG CII ი მმც E GAT CCT ව පිරිපි V GTG E K AAG V GTG R AGG K AAG ဗ္ဗဗ္ဗ CCC A GCC A GCC Д GAC DGAC E r CTG CCC g G C C CTG E GAA T ACG W TGG AGG V GTG E GAG F TTT ద ATG R AGG L CTG W TGG r CTG r CTG F TTT s AGC ဗ္ဗ A GCC GAC EGAG GAC r CTC CIC GAG N AAC GTG r CCC A GCC GAA V GTG A GCC R AGG L CTG CŢĠ සි පි > LCTG CTC A S Y TAC မှု ည r GTG F A GCC A R AGG $_{\rm L}^{\rm L}$ ი მმც E

R AGG FCC ACG S AGT Y TAT IATC F IATC ^Р ССС Y A V GTG R AGG A Si E r CHC L CAG CAG DGAC r CTG M ATG ACC. ი მვ CTA F ස විව ۳ C E R AGG ი მმმ r CTG N AAC WTGG K AAG GCC မှ ည L E နှင့်င සි r CTT V GTC ය විව H ဗ္ဗဗ္ဗ LCTT A GCC E GAG s AGC A GCC CAG CAG CAG R AGG GAG G GGG R AGG CTA Y IATC T ACG P V GTG D GAC A GCC s TCC F TTT A GCC A GCG E L GAG CTA O CAG CIC ဗ္ဗဗ္ဗ GAC A GCC A GCC T ACC r TTG д GGC T R CGG L CTC Y TAC D GAC (T ACG (S AGC (CTG CCA R GGC LCTA S TCC E GAG R CGC GGC BBC R GGC E GAG Д P CCG I ATC A GCC v GTC T ACC W TGG T ACG M ATG CAC E EGAG CIC V GTG I V E K ATC GTG GAG AAG S T ACG r TTG CCC g GGG CAC H r CTG A GCC I ATT r CTG TAC × F N Q TTC AAC CAG 1 I D P ATT GAC CCC K R AAG CGC N I AAC ATC R E GAG A GCC IATC CCC T ACC s TCG F TTC CTC E GAG GAC ය විට V GTC r CTG DGAC M ATG A GCC A.A.G ස ස CAG V GTG R AGG A GCC R CGG V GTG ი მმშ CAG E GAG යියි 7 CCC 7 GAA CTC ဗ ဗ္ဗ Y TAC CGC CGC I ATC I ATT E K T GAG AAG ACC ი მმი A GCC Y TAC A GCC r Agg CAC T ACC TGG. F ACC AAC \mathbf{F} E CTG r CHC E GAG CTC E A GCC S AGC CAC CAG P gcc Gcc e Gag CAG R V GTC E gcc Gcc CHC CHC E K AAG I ATA T ACG CHC D GAT T ACC GAC cgg F ည် ი გე Y ය පුව K AAG GGC BC L CTG က္လင္သ s TCC က္ခင္လ Q CAG V GTC V GTC $_{
m TTC}$ PCCT V GTG GAG ggc 7 ဗ္ဗဋ္ဌ AAC s TCC CIC ဗ ဗ္ဗ s AGC S AGC ය විව IATC K AAG IATC K AAG V GTG

တ္မွ EGAG A GCC ი გე V O GTC CAG M E ATG GAG r CTG E GAG r STO R AGG က်င္သင္သ V GTC V GTC CCC R E A A E R M A F N M CGG GAG GCC GAG CGC ATG GCC TTC AAC ATG r CTG E F D E GAC GAG (A K GCC AAG K L AAG CTC r Great L M K L A M V CTC ATG AAG CTG GCT ATG GTG CAC V GTC GG P CAG A E A V A GCG GAG GCC CTT CTC R M AGG ATG E R GAG AGG GAC A GCC v GTG A GCC ი მმმ K S AAG AGC (T A A A A A C GCC P K CCA AAA E M GAA ATG

W CAT E D GAG GAC' H H R G G G G H CGC GGC GGC CAT A V P L E V E V G I G GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG L S A K B G I D G CTC TCC GCC AAG GAG GGC ATT GAT GGC r CTG GCC CCC V Y GTG TAT

H H * CAT CAT TAA

Figure 17GGG

Pfu DNA Polymerase (WT) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 71)

//

totaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat caactctaca cotococtat tttototott atgagatttt taagtatagt tatagagaag ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc ccccagtcgc gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga

FIGURE 17GGG (CONT.)

ttacataact gaagaaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaact tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga agtagotoca aacaagocaa gtgaagagga gtatcaaaga aggotcaggg agagotacac aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct aataccaatg gaggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct tcacgaagga

FIGURE 17GGG (CONT.)

tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaagc gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa aggogatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc

FIGURE 17GGG (CONT.)

tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt tttgetecaa geagageege tecaatggat aacaeeeetg tteeegeaee caagteeget acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct ttccggggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnn nngtcctctc ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa gtagaagcgg cactactcag atgettecee aggaatgagg ttgttgtage tentecenga aagattgaga tgttcttgg // // GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG AAG GAG CTG TGA : CTG CAG ATG CTG GAG AAG CAG AAA AAG

Figure 17HHH

PFU DNA POLYMERASE (V93 R OR E) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 71)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 1020 1200 1260 1320 1380 1440 1500 1080 1140 960 900 TCTIGCCTIC TGTATATGAA TGGACAACCT ACTTAGGAAA TCAAAGAAGG AGTAGGCCAC GGGAAGAAAG CATTTACGCT TAACGGGGA AAGGCATGGA CAAGCCTATT AAAGAGATAC TATAATGATT TATCAGGGAG AGCCTGGGAA GGCAACTTAT CAATGTTTCT GTTAGAGGAA AGAAAAGTT TCTTCCATAC ATATTAGCG CGAGCCCAAG TTTCGACTTG GTGGGAAAAC AATACTCCTT TTAIGGCIAT **AAAGAAAAAG** CTGTTATTAG GCTATTCAAA CCTCTACATT GLUTAMIC ACID) AAGGCCCAAT GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAACATAGA TCGCATTCCC CAAGATTAGT TITCAAGGIC AAGCACAGGG AACCIIGIAG AGIGGIICII TTAGACCATA AGTTTCTCGG CCACTATTAG AGCTAAAGAT TTCTCAGGAT AAGAGGAGTA TTCCATTTGC GAGATGGAAG GAAGAATACA CACTAGAGGC AGATAGCAAA AAGATGCAAA AAAAGGGGTT TCGCTCCTCA CTATAGAAAA TCTACGGATA TTACTGCCTG TAATTACCCA TGGGACATTT GATTTAAAGT V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GTTAAGAAAA GTTGAGAAAA GGGGAAGAAG GAGTTTGGAA ATTACTTGGA GGAGACTCAT ACCATTGGAA GAAGTCAAGG TACTCGATGG TCCAATGGAA ATTCAGCTTT AAGCCAAGTG AAAGAGCCAG GCTGAGAGCG GAAAAGTTTG ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC GATAGAACTT CAAGATXXXC GAATACGATA ATAAAGAGAT TACGCCGACG CCCTCGATTA AACTATGATA CCAAGTCTCT ACTCAAGATC V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CCAACATACA GCAAATTCTT GAAAATTTAA GATAGAGCAT AGCAAAGGTG AGCTCCAAAC ATGATTCAAA GATTGAAGAA GGACATCTTC TACTTATAAT GGGATGCAAG AATGAAGGAA TGTAGAGAAG CGAAGGAGAA GAGAGAGATG GATTAAATTA GACGGCTGTA AATAAATCTC GGAGAAGGTA AGTTGCCAAA TGGATTCGTT AGCCCTATAT GATGGTACTG TAAGGAGTGT TAGTATGGAA GGAGCTCGAA GGAACATCCC ACCAATGGAG TGGTTTTATA AAAACTCTTA ATGAAAATGA TAACAAGGAC GAAACGAAGT TAGATTTTAG GAATTGTTGA CAGCAGTTGT AAGGCCTAAT CCCTCTATCA ACATTATAGT AAAAACTTGG TAGGCGATAT ACCTTGAGAG AAGAATTCCT AGGACATCCC TTAAGACAAA AACTTTATTT TATCAAGCGA GAAAGCCAAA GCTACACAGG TAAATCTTGA AAAAAGCGAT CTTCTCAGGG AAAGAGAACG AAGATTGTGA ACCGTGTGGA AGTTATGCAG AAGTTCTGCA SACTATAGAC TACATCGAGT GACACTGATG CTCATCGACA AAGGATCCTG AAAAGGGCAG ATGCAGAGAA GCCTACGAAA CTCAGGGAGA ATAGTATACC CCCGATACTC AGACAAAAGA AGAGAACATC GATATAGAAA GTTGAGGTTG TATCATGTAA GCAATTTTTG AGTGGAGAGA GAACTCGGGA TTATGGGATG GCAAAAGCAA

FIGURE 17HHH (CONT.)

GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG ACC TAC GAC GAG 1980 2040 2100 2160 GAC ATC GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG AGCTGAGGAA TGAAGAAGCT CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC AATAGATGAA AATGGTAATT GGTTCTTCCA TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT TGAAATTGCA GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA ATAAGAGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TTTGGAGACA ATACTAAAAC ACGGAGATGT CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GTG GGC AAG ATG ATC TCC TTC TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC 2328 ATG CTG GAG AAG CAG AAA AAG CGI AAG ACC GGC CGT AAA GTA TGG AAGCTAGAGT TACTTAGAGG ACAAGACAAG CTG CAG ATC AAG GAAGGGTTTT GTAGCTGTTG GGATACATAG GCGGTACTTA // GCA ACC GGT GGC GCTCTAGAAT GAAGGAAAAG AAAGAAACTC TACGATCCCA

Figure 17III

PFU DNA POLYMERASE (G387P/V93R OR E) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 71)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 387P Mutant (CCN is the codon for Proline where N = C, G, A, or T) AGCAAAGGIG ATTACTIGGA AAAACAIAGA ICTICCAIAC TATCAGGGAG AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG AFGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT AAGGCATGGA AGAAAAAGTT CAGCAGTIGI GGACATCTIC GAATACGATA ITCCATTIGC AAAGAGATAC CAAGCCTATT TATAATGATT TCTTGCCTTC V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) TAACGGGGGA GAGAGAGATG ATAAAGAGAT TICTCAGGAT GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGATXXXC CCACTATTAG CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT GAGTTTGGAA AAGGCCCAAT CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, GGAACATCCC CGAAGGAGAA AACTTTATTT ATGAAAATGA CCCTCTATCA TATCAAGCGA ACCGTGTGGA AGAGAACATC GTTGAGGTTG AAGATTGTGA GATATAGAAA AGTTATGCAG

FIGURE 17III (CONT.)

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1500
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                                                                              1140
                                                                                                          1260
                                                                                                                       1320
                                                                                                                                    1380
                                                                                                                                                  1440
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                                                                                                                                                                                            1620
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                                                                                                                                                                                                                                   1800
                                                                                                                                                                                                                                                 1860
                                                                                                                                                                                                                                                              1920
                                                                                                                                                                                                                                                                           1980
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                                                                                                                                                                                                                                                                                                       2100
                                                                                                                                                                                                                                                                                                                    2160
                                                     1020
                                                                  1080
                                                                                             1200
                                                                                                                                    GTTAGAGGAA
                                                                                                                                                                             GGGAAGAAAG
                                                                                                                                                                                                        AAAGAAAAAG
                                                                                                                                                                                                                     GCTTGAATAT
                                                                                                                                                                                                                                   AATAGATGAA
                                                                                                                                                                                                                                                                                                                     AGCTGAGGAA
                                                                                                                                                                                                                                                                                                                                  GGTTCTTCCA
TTTCGACTTG
                                                     TGGACAACCT
                                                                  ACTTAGGAAA
                                                                              TCAAAGAAGG
                                                                                                          CAATGTTTCT
                                                                                                                        AGTAGGCCAC
                                                                                                                                                  AATACTCCTT
                                                                                                                                                                TTATGGCTAT
                                                                                                                                                                                            CCTCTACATT
                                                                                                                                                                                                                                                 TGAAATTGCA
                                                                                                                                                                                                                                                              TGAAGAAGCT
                                                                                                                                                                                                                                                                           ACCAGAGAAG
                                                                                                                                                                                                                                                                                          AGGTCCTCAC
                                                                                                                                                                                                                                                                                                       AATGGTAATT
                                                                                                                                                                                                                                                                                                                                                ATACCAAAAG
             TGTATATGAA
                         AGCCTGGGAA
                                       GGCAACTTAT
                                                                                             GTGGGAAAAC
                                                                                                                                                                                                                                                                                                      GGAGTTAAAA TAAAGCCAGG
                                                                                                                                                                                                                                                                                                                                               TACAGAAAGG AAGACCTCAG
GAAGAATACA
           CACTAGAGGC
                         AGATAGCAAA
                                                                              AAGAGGAGTA
                                                                                            AAAAGGGGTT
                                                                                                                        TCGCTCCTCA
                                                                                                                                    TGGGACATTT
                                                                                                                                                                TCTACGGATA
                                                                                                                                                                             TTACTGCCTG
                                                                                                                                                                                           GATTTAAAGT
                                                                                                                                                                                                        GTGAGGAAAT
                                                                                                                                                                                                                                  GGTATGCAGT
                                                                                                                                                                                                                                                                           ATGAAATTCC
                                                                                                                                                                                                                                                                                         ATAAGGCGAT
                                                                                                                                                                                                                                                                                                                   GGGCAATTCT
                                                                                                                                                                                                                                                                                                                                 GTATGACGCA GAATATTACA TGGAGAACCA
                                       AAGATGCAAA
                                                     CAAGATTAGT
                                                                  AGTGGTTCTT
                                                                                                                                                   CTATAGAAAA
                                                                                                                                                                                                                    GACTGCTAGA
                                                                                                                                                                                                                                                 GAGATTGGAG
                                                                                                                                                                                                                                                             ATACTAAAAC ACGGAGATGT
                                                                                                           TAATTACCCA
                                                                                                                                                                                                                                                                                                                                                             TTCCTGGCTT AACATTAAAA AATCC //
GAAGTCAAGG
                                                                 AACCTTGTAG
                                                                                            AAAGAGCCAG
                                                                                                                                                                             GCTGAGAGCG
                                                                                                                                                                                           GAAAAGTTTG
                                                                                                                                                                                                                                                                           CTTGCCAATT
                                                                                                                                                                                                                                                                                         TTACATGAGT
                         TACGCCGACG
                                       TACTCGATGG
                                                                              AAGCCAAGTG
                                                                                                                       AACTATGATA
                                                                                                                                                                                                                                                                                                                     ATTAGCAATA
                                                    TCCAATGGAA ATTCAGCTTT
                                                                                                          CCCTCGATTA
                                                                                                                                    CCAAGTCTCT
                                                                                                                                                                                                         GGAGGAGAAA
                                                                                                                                                                                                                     AAGCTCCCTG
             CCAACATACA
                                                                                                                                                   ACTCAAGATC
                                                                                                                                                                GCAAATTCTT
                                                                                                                                                                                                                                                 TGGTTTAGAG ATAGTTAGGA
                                                                                                                                                                                                                                    ACGAAGAAGA
                                                                 AAGCACAGGG
                                                                                                                       GGGATGCAAG
                                                                                                                                                                                                                                                             TTTGGAGACA
                                                                                                                                                                                                                                                                                                                                               GGGATTTGGA
                                                                                                         AGCCCTATAT
                                                                                                                                                   AATGAAGGAA
                                                                                                                                                                                                        AACTATCCCA
                                                                                                                                                                                                                                                                                                                     CGATGGTCCA
GACGGCTGTA
                          GGAGAAGGTA
                                       AGTTGCCAAA
                                                                              AGCTCCAAAC
                                                                                             NGGATTCGTT
                                                                                                                                     TGGTTTTATA
                                                                                                                                                                AAAACTCTTA
                                                                                                                                                                            TAAGGAGTGT
                                                                                                                                                                                           GGAGCTCGAA
                                                                                                                                                                                                                     CATAAATTCA
                                                                                                                                                                                                                                   ATTCTTCGTT
                                                                                                                                                                                                                                                                           AATACAAAAG
                                                                                                                                                                                                                                                                                         AACAAGACCA
                                                                                                                                                                                                                                                                                                       AGCTGCTAAA
             AATAAATCTC
             TAACAAGGAC
                                                    AAGAATTCCT
                                                                                                                                                   TTAAGACAAA
                                                                                                                                                                                                                                                                           TAAAAGAAGT
                                                                                                                                                                                                                                                                                                                                  TACGATCCCA AAAAGCACAA
                                                                                                                                                                                                                                                                                                                                               GGATATTGGA
                                                                                                                                                                                                                                                                                                                                                             TCGGCCTAAC
                                                                  TTTCAAGGTC
                                                                                                                                    AGGACATCCC
                                                                                                                                                                AAAAAGCGAT
                                                                                                                                                                                            TAGTATGGAA
                                                                                                                                                                                                         GTCTCTATGC
                                                                                                                                                                                                                     TTGTAAAATA
                                                                                                                                                                                                                                    ATAAGAGGGG
                                                                                                                                                                                                                                                 TCATTACTCG
                                                                                                                                                                                                                                                               AAGCTAGAGT
                                                                                                                                                                                                                                                                                         ATGAGCAGAT
                                                                                                                                                                                                                                                                                                       CAAAGAAACT
                                                                                                                                                                                                                                                                                                                     TACTTAGAGG
TAGGCGATAT
                         GAAAGCCAAA
                                       ACCTTGAGAG
                                                                              GAAACGAAGT
                                                                                             GCTACACACC
                                                                                                                      TAAATCTTGA
                                                                                                                                                                               GATGGTACTG
                                                                                                           TAGATTTTAG
             TATCATGTAA
                                                                                                                                                                                                                                                                                                                   GGATACATAG
                                                                                                                                                                                                                                                                                                                                                             ACAAGACAAG
                                                                 TTATGGGATG
                                                                                                                       CCCGATACTC
                                                                                                                                     AAGTTCTGCA
                                                                                                                                                   AGACAAAAGA
                                                                                                                                                                                                        GACACTGATG
                                                                                                                                                                                                                     GCTCTAGAAT
                                                                                                                                                                                                                                                              AAAGAAACTC
                                                                                                                                                                                                                                                                           GTGAGAATAG
                                                                                                                                                                                                                                                                                         CTCGCAATAT
                                                                                                                                                                                                                                                                                                                                                GCGGTACTTA
ATGCAGAGAA
                                                     GAACTCGGGA
                                                                               GCCTACGAAA
                                                                                             CTCAGGGAGA
                                                                                                         ATAGTATACC
                                                                                                                                                                GACTATAGAC
                                                                                                                                                                                           TACATCGAGT
                                                                                                                                                                                                                                                 GAAGGAAAAG
                                                                                                                                                                                                                                                                                                      GIAGCIGITG
                          GCAATTTTTG
                                       AGTGGAGAGA
                                                                                                                                                                              GCAAAAGCAA
                                                                                                                                                                                                                                    GAAGGGTTTT
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TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG ACC TAC GAC GAG GTG GGC AAG ATG ATC TCC TTC TGA CAG AAA AAG GGT CGT CGI TTC AAG GAG AAG TGG AAG ACC GGC CTG GTA AAG ATC AAG AAA GTA ATG // GCA ACC GGT GGC CTG CAG

Figure 17JJJ

PFU DNA POLYMERASE (D141A/E143A/V93R OR E) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 71)

FIGURE 17JJJ (CONT.)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGT (ALL POSSIBLE CODONS FOR ARGININE) G, A, or T) 1560 1500 1380 1620 1740 1800 2100 1020 1080 1140 1200 1260 1320 1440 AAAGAAAAG 1680 1860 1920 1980 2040 840 900 960 480 540 TGTATATGAA CAATGTTTCT GGGAAGAAAG GCTTGAATAT TGAAATTGCA TGAAGAAGCT ACCAGAGAAG AGGTCCTCAC AATGGTAATT AGCTGAGGAA CAAGCCTATT AGCCTGGGAA TGGACAACCT ACTTAGGAAA TCAAAGAAGG AGTAGGCCAC GTTAGAGGAA AATACTCCTT CCTCTACATT GGTTCTTCCA CATTTACGCT AAGGCATGGA TCTTCCATAC ATATTTAGCG CGAGCCCAAG TTTCGACTTG GGCAACTTAT GTGGGAAAAC TTATGGCTAT AATAGATGAA AGAAAAAGTT TCTTGCCTTC TATAATGATT TATCAGGGAG ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA AAAGAGATAC D141A/E143A Mutant (GCN is the codon for alanine where N = C, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TITCAAGGIC AAGCACAGGG AACCITGIAG AGIGGIICIT CTTGCCAATT ATGAAATTCC TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CCACTATTAG GAAGAATACA CACTAGAGGC GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA CTATAGAAAA GTGAGGAAAT GAGATTGGAG ACGGAGATGT GGGCAATTCT GAATATTACA TGGAGAACCA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT ATTCAGCTTT CAAGATTAGT TCTACGGATA TTACTGCCTG GATTTAAAGT GACTGCTAGA GGTATGCAGT ATAAGGCGAT TAAAGCCAGG TTAGACCATA TTCCATTTGC AGCTAAAGAT AGCAAAGGTG ATTACTTGGA AAAACATAGA TCGCATTCCC GAGATGGAAG TACTCGATGG AAGATGCAAA AAAAGGGGTT TAATTACCCA TCGCTCCTCA TGGGACATTT GAATACGATA GGGGAAGAAG GGAGACTCAT ACCATTGGAA GAAGTCAAGG CCAACATACA AAAGAGCCAG CCCTCGATTA TAAATCTTGA GGGATGCAAG AACTATGATA CCAAGTCTCT TTAAGACAAA AATGAAGGAA ACTCAAGATC GCTGAGAGCG GAAAAGTTTG GGAGGAGAAA CATAAATTCA AAGCTCCCTG TGGTTTAGAG ATAGTTAGGA TTTGGAGACA ATACTAAAAC TTACATGAGT TACTTAGAGG CGATGGTCCA ATTAGCAATA CAAGATXXXC GCAAATTCTT ACGAAGAAGA GGAGTTAAAA GATAGAACTT TCCAATGGAA AAAGAGAACG GAAAATTTAA GATAGAGCAT TACTTATAAT GATTAAATTA GACGGCTGTA AATAAATCTC ACCTTGAGAG AGTTGCCAAA GCTACACA GTTGGATTCGTT TAGATTTTAG AGCCCTATAT AGGACATCCC TGGTTTTATA AAAAAGCGAT AAAACTCTTA TAAGGAGTGT GTCTCTATGC AACTATCCCA ATTCTTCGTT ATGAGCAGAT AACAAGACCA racgarcca AAAAGCACAA GTATGACGCA ACCGIGIGGA AACTITATIT GGAACAICCC CAGCAGTIGT GGACATCTIC ACCAATGGAG GGAGCTCGAA TAAAAGAAGT AATACAAAAG AGCTGCTAAA AAGATTGTGA GAATTGTTGA CCCTCTATCA TATCAAGCGA TAGGCGATAT TAACAAGGAC AAGAATTCCT GATGGTACTG TTGTAAAATA ATAAGAGGGG AAGCTAGAGT CAAAGAAACT AAGGCCTAAT ATGAAAATGA ACATTATAGT AAAAACTTGG TAGTATGGAA TCATTACTCG AAGTTCTGCA TTATGGGATG CCCGATACTC AGACAAAAGA GAAGGAAAAG AAAGAAACTC GTGAGAATAG GGATACATAG AGTTATGCAG AAGGATCCTG AGTGGAGAGA ATAGTATACC GACTATAGAC TACATCGAGT GCTCTAGAAT CTCGCAATAT AGAGAACATC CTCATCGACA GCNATAGCNA AAAAGGGCAG ATGCAGAGAA TATCATGTAA GAACTCGGGA GCCTACGAAA CTCAGGGAGA GCAAAAGCAA GACACTGATG GAAGGGTTTT GTAGCTGTTG GTTGAGGTTG GCAATTTTG

FIGURE 17JJJ (CONT.)

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ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
                                                                                                                                                                          GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
                                                                                                      GAC ATC TCC
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
                                                                                                         AAA GGC GAA GAA AAA GAG GTA
                                   ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
                                                                                                           TAC
                                                                                                                                                                               GGT GGC AAG ACC GGC CGT
                                                                                                           TTC AAG
                                                                                                           // GCA ACC GTA AAG
```

// TGA

CTG CAG ATG CTG GAG AAG CAG AAA AAG

Figure 17KKK

KOD DNA POLYMERASE - Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 71) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

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1020
                                                                                                                                                                                                                                                                                                                                                                1080
                                                                                                                                                                                                                                                                                                                                                                                    1140
                                                                                                                                                                                                     600
                                                                                                                                                                                                                                                                                   840
                                                                                                                                                                                                                                                                                                                                                                                    GGCCAGAAGA
                                                                                                                                                                                                                                                                                 CGTTTATGAA
                                                                                                                                                                                                                                                                                                                                                                CCTCAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                      GGAGAACATA
                                                            ACGATICIGC CATIGAGGAA GICAAGAAGA TAACCGCCGA GAGGCACGGG
                                                                              ACGGITGIAA CGGITAAGCG GGITGAAAAG GITCAGAAGA AGITCCICGG GAGACCAGII
                                                                                                GGACAAGATA
                                                                                                                                                                                                                                                                                                     AGCCTGGGAA
                                                                                                                                                                                                                                                                                                                                            CGGCCAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGCCACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAGGAGAGG
                     ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG
                                         TIGAACCCIA CITCIACGCC
                                                                                                                                                                                TCTCCCCTAC
                                                                                                                                                                                                     TGTGAAGGAG
                                                                                                                                                                                                                                                               CTTCGATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                           CGTCTCGCCG
                                                                                                                    CAAGCGCTAC
                                                                                                                                          GCTCGCCTTC
                                                                                                                                                              CCTTATGATA
                                                                                                                                                                                                                       CTATCTGAAA
                                                                                                                                                                                                                                           CGAGCCGAAG
                                                                                                                                                                                                                                                                                                                         GGTCACATAC
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
                                                                                                                                                                                GGCCAGGGTG ATAACTTGGA AGAACGTGGA
                                                                                                                                                                                                                                                                                                                                           CTCGCTTAAT
                                                                                                                                         AGCTGAAAAT
                                                                                                                                                            TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT
                                                                                                                                                                                                    GAGGGAGATG ATAAAGCGCT TCCTCCGTGT
                                                                                                                                                                                                                                                                                 CGCTTGAGGC
                                                                                                                                                                                                                                                                                                     AAATAACCAC
                                                                                                                                                                                                                                                                                                                        AAGATGCGAA
                                                                                                                                                                                                                                                                                                                                                              AGTGGTTCCT
                                                                                                                                                                                                                                                                                                                                                                                  GGCCCCGAAC AAGCCCGATG AAAAGGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                      GAGGGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT
                                                                                                  CAGCGATAAG
                                                                                                                      TACCCTTCGC
                                                                                                                                                                                                                       TCGACTTCGC
                                                                                                                                                                                                                                           GGGATGGAAG
                                                                                                                                                                                                                                                              GACGGATACA
                                                                                                                                                                                                                                                                                                                                                                                                                          TCACCCACAA
                                                                                                                                                                                                                                                                                                     TACGCTGAGG
                                                                                                                                                                                                                                                                                                                                                                 CAGCACTGGC AACCTCGTTG
                                                                                                                      TGACATCTAC GAGTACGACA
                                                                                                                                         GCCAATGGAA GGCGACGAGG
                                                                                                                                                                                                                                                                                                                        TACTCGATGG
                                                                                                                                                                                                                                                                                                                                              TCCGATGGAG GCCCAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                      CTATGTAAAA GAGCCCGAGA
                                         AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT
                                                                                                 GAGGICTGGA AACTCTACTT TACTCATCCG CAGGACXXXC
                                                                                                                                                                                                                       GGCGACAACT
                                                                                                                                                                                                                                           AATAAACTTC GCCCTCGGAA
                                                                                                                                                                                                                                                              GTTTGCCGTC GAAGTGAAGG
                                                                                                                                                                                                                                                                                 GATAAACCTG CCCACATACA
                                                                                                                                                                                                                                                                                                                                                                                                                          TCAATCATCA
                                                                                                                                                                                                                       ACGITCICAL AACCIACAAC
                                                                                                                                                                                                                                                                                                     GGAGAAGGTT
                                                                                                                                                                                                                                                                                                                        AGTCGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                          CCTGTACCCC
                                                                                                                      CAGCAGTTAT
                                                                                                                                                                                                                                           AAAAGCTCGG
                                                                                                                                                                                                                                                               TGGGCGACAG
                                                                                                                                                                                                                                                                                 TAAGACGGAC
                                                                                                                                                                                                                                                                                                                        ACCTTGAGAG
                                                                                                                                                                                                                                                                                                                                            AGGAGTTCCT
                                                                                                                                                                                                                                                                                                                                                                                    GCCTATGAGA GGAATGAGCT
                                                                                                                                                                                                                                                                                                                                                                 TCTCCCGCTC
                                                                                                                                         AGGGATTAGT
                                                                                                                                                              CTCTCTACCA
                                                                                                                                                                                ACGAGGAAGG
                                                                                                                                                                                                     TCTCGACGGA
                                                                                                                                                                                                                                                                                                      GTCAGCCGAA
                                                                                                                                                                                                                                                                                                                                                                                                        ATGAAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                          ATTTAGATC
                                                                                                                                                                                                                                                                                 TATCCTGTGA
                                                                                                                                                                                                                                                                                                                                                              CTCTGGGACG
                                                                                                                                                                                                                                                                                                                                                                                                      CGGCAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                              GATACGCTCA
                                                            CTCCTGAAGG
                                                                                                                                         CTCATAGACA
                                                                                                                                                                                                     GTTGACGTCG
                                                                                                                                                                                                                                                                                                                         ACCGGCGAGA
                                                                                                                                                                                                                                                                                                                                            GAGCTTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                          GTGTACCTAG
                                                                                                                      CGAGAGCATC
                                                                                                                                                              GACATTGAAA
                                                                                                                                                                                AGCTACGCCG
                                                                                                                                                                                                                         AAAGACCCGG
                                                                                                                                                                                                                                           AAGCGCTGTG
                                                                                                                                                                                                                                                                                                       GCCGTCTTCG
                                                                                                                                                                                                                                                                 ATTCAGAGGA
```

FIGURE 17KKK (CONT.)

```
1680
                                                                                1740
                                                                                               1800
                                                                                                               1860
                                                                                                                               1920
                                                                                                                                                1980
                                                                                                                                                                2040
                                                                                                                                                                                2100
                                                                                                                                                                                                2160
                                                1620
                                                               AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT
                                                                              CGAGTACGAG
                                                                                                                                                                                                CGACGAGTTC
                                                                                                                                                                                                                              CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG
              CGGCTATGCA
                                                                                               AGACGAGGAA
                                                                                                               GATAGCGAAA
                                                                                                                                                GGAGAAGCTG
                                                                                                                                                                               GGTGATAAGC
                                                                                                                                                                                                                TCTCCCAGCC
 GCTCCTCGAT
                               AAGGGAGTAC
                                                CTACAGCGAC
                                                                                                                                GAAGGCCGTG
                                                                                                                                                              TCCCCACGIT
GAAGGCCACG ATTGACCCGA TCGAGGGAA
               GATCCTGGCA AACAGCTACT ACGGTTACTA
                               CGGCCTGGGG
                                              TTAAGGTAAT
                                                                              CAACGCCAAA CTTCCGGGCG CGCTTGAGCT
                                                                                                CTTCGTCACG AAGAAGAAGT ATGCGGTGAT
                                                                                                               ACTGGAGCGA
                                                                                                                                                              GAGGGATTTA AAGGACTACA AGGCAACCGG
                                                                                                                                                                                                               CGACGCCGAG TACTACATTG AGAACCAGGT
                                                                                                                                               AGCAAGTACG AGGTTCCGCC
                                                                                                                                                                               GCCCTGGAAC
                                                                                                                                GTGACGTCGA
                                                                                                                                                                                                CGATACCGTT
                                                                                                                                                                                                                                               TIGGCIGAAG CCGAAGGGAA CT 2325
                                                                                                               GTGAGGCGTG
                                                                                                                                CTAAAGGACG
                                GGAGTGTGCA GAGAGCGTAA
                                               AAGTACGGCT
                                                                                                                                                                               CGCGAGAGGA GTCAAAATAC
                                                                                                                                                                                                GGCGACAGGG
                                                                                                                                                CGAAAAGCTG
                                                                                                                                                                                                TGGGAGGATA
                                                 GATAGAGGAA
                                                                                                               ACTTGAGATT
                                                                                                                                TGAAGCTTTG
                                                                                                                                                                                                                                                GTTTGAGTGC
                                                                                                                                                                                                                               TTCTGAGAGC
   AGAAGAAGAT
                 GGGCCATCAA
                                GGTACTGCAA
                                                CCATCAAGGA
                                                                TTTTGCCAC
                                                                                                AACGCGGCTT
                                                                                                                 CAACGCGCGG
                                                                                                                                 CGAGGGTTCT
                                                                                                                                                 AAGAAGTTAC
                                                                                                                                                                AGCAGATAAC
                                                                                                                                                                                 AGAGGTTGGC
                                                                                                                                                                                                TCAAGGGCTC
                                                                                                                                                                                                                 AGCACAAGTA
                                                                                 TCAAGTATAT
                                                                                                                                                                                                                                  GTTGAGAGAA
   CAGAAGATAA
                                                                ACCGACGGAT
                                                                                ATGGAGTTCC
                                                                                                  GGCTTCTACA
                                                                                                                 GGCAAGATAA
                                                                                                                                                                 GTGATCCACG
                                                                                                                                                                                  GCCGTTGCCA
                                                                                                                                                                                                TACATCGTGC
                                                                                                                                                                                                                 GACCCGACGA
                                                                                                                                                                                                                                                 AGACAGGTTG
                   TACAGGCAGA
                                 AGGCGCGCT
                                                ATAACGATGA
                                                                                                                                 GAGGCGCAGG
                                                                                                                                                  AGGATAGTCA
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ggG CTG GAC ATC TCC ATC TCC TTC ACC TAC GAC GAG GAA AAG GAC GCG CCG AAG GAG GTA GAA AAA GAG TAC AAA GGC GAA GTG GGC AAG ATG GGT GCG GTA AGC CAG AAA AAG // CGT CGT AAG CTG CAG ATG CTG GAG AAG GTA TGG GGT GGC AAG ACC GGC AAG AAA ATC AAG ACC GCA

Figure 17LLL

Sso7d - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 33) Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 34) CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) CGA, CGC, CGG, V93R MUTANT: XXX = AGA, AGG,

GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAA AAG GGC CGT GGT CAG AAG TAC CGT GTG AAG GAG TTC TGG CTG GTA GTA AAG GGT GGC AAG ACC ATC AAG AAA CAG ATG //GCA ACC CTG

FIGURE 17LLL (CONT.)

1260 1380 1620 1680 1020 1080 1140 1200 1320 1440 1500 1560 1740 1800 1860 1980 2040 2100 //ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60 840 540 900 960 AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120 CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180 AGACGAGGAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA GATAGCGAAA TCCCCACGTT CCTCAGGAAG GGAGAACATA AAAGAAGGCT GAAGGCCGTG GGAGAAGCTG GGTGATAAGC TCTCCCAGCC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG CAGCGATAAG GGACAAGATA CAAGCGCTAC CCTTATGATA CGTTTATGAA CGGCCAGTCC GGCCAGAAGA CGTCTCGCCG AGAGGAGAGG GCTCCTCGAT AAGGGAGTAC CTACAGCGAC CGAGTACGAG CGACGAGTTC GCTCGCCTTC TCTCCCCTAC TGTGAAGGAG CTATCTGAAA CGAGCCGAAG CTTCGATCTC AGCCTGGGAA GGTCACATAC CGGCCACCGC CT //TAG 2325 CGGCCTGGGG ATGCGGTGAT AAACCGTCAA TACTACATTG AGAACCAGGT TCGAGAGGAA CGCTTGAGCT GTGAGGCGTG ACTGGAGCGA AGGTTCCGCC AGGCAACCGG GCCCTGGAAC CGATACCGTT GTTCAGAAGA AGTTCCTCGG CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC GGCGACGAGG AGCTGAAAT TCCTCCGTGT GACGGATACA AAATAACCAC AAGATGCGAA CTCGCTTAAT GAGGGTTGTG TCACCCACAA GAGACCTCCT TTAAGGTAAT GTGACGTCGA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT AGAACGTGGA TCGACTTCGC GGGATGGAAG CAGCACTGGC AACCTCGTTG AGTGGTTCCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT CCCCACAGGT CGCTTGAGGC AGTCGCCCGC TACTCGATGG GCCGATGCTG CTTCCGGGCG AAGAAGAAGT AGCAAGTACG AAGGACTACA GTCAAAATAC TTGGCTGAAG CCGAAGGGAA AGCCTGCTTG CTAAAGGACG GGCGACAGGG AACTCTACTT TACTCATCCG CAGGACXXXC TACGCTGAGG TCCGATGGAG GCCCAGCTTT CCTGTACCCC TCAATCATCA ATTGACCCGA GGAGTGTGCA GAGAGCGTAA GATAGAGGAA AAGTACGGCT ATAACTTGGA ATAAAGCGCT GGCGACAACT GAAGTGAAGG CCCACATACA GAGCCCGAGA TATGACGTTG GCCCTCGGAA GAGGGATTTA CTATGTAAAA ATGCAAGGAA ATTTATCCCG GAAGGCCACG CTTCGTCACG CGAAAAGCTG CTTCGGTTAC AATACCTGGA CGCGAGAGGA TGGGAGGATA GGTTGAAAAG GGCCAGGGTG GAGGGAGATG AACCTACAAC GGAGAAGGTT CAACGCCAAA ACTTGAGATT TGAAGCTTTG CGACGCCGAG GCCAATGGAA AATAAACTTC GTTTGCCGTC GATAAACCTG ACAGAGAAGG ACTTCCCAGG CAACGCGCGG GTTTGAGTGC AAAAGCTCGG AGGAGTTCCT AGAAGAAGAT GGGCCATCAA CCATCAAGGA TTTTTGCCAC TCAAGTATAT AACGCGGCTT AGAGGTTGGC ATGAAGGAGG ATTTAGATC AAGAAGTTAC AGCAGATAAC TCAAGGGCTC AGCACAAGTA TTCTGAGAGC CGGTTAAGCG ACGTTCTCAT TGGGCGACAG GTCAGCCGAA ACCTTGAGAG TCTCCCGCTC GGAATGAGCT GGTACTGCAA CGAGGGTTCT AGGGATTAGT CTCTCTACCA ACGAGGAAGG TCTCGACGGA TAAGACGGAC GATACGCTCA GGCTTCTACA GACCCGACGA GTTGAGAGAA TTCTGCAAGG AGGATAGTCA GCCGTTGCCA TACATCGIGC SAGGTCTGGA GAGCTTGGGA CTCTGGGACG GTGTACCTAG CAGAAGATAA TACAGGCAGA AGGCGCGCT ATAACGATGA ACCGACGGAT GTGATCCACG AGACAGGTTG ACGGTTGTAA CGAGAGCATC CTCATAGACA AGCTACGCCG AAAGACCCGG AAGCGCTGTG TATCCTGTGA GCCGTCTTCG ACCGGCGAGA GCCTATGAGA CGGCAGAGCT ATGGAGTTCC GGCAAGATAA GAGACGCAGG GACATTGAAA GTTGACGTCG ATTCAGAGGA

Figure 17MMM

Sso7d-Vent DNA POLYMERASE FUSION PROTEIN

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Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 35)
                                                                                    Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 36)
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CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG,

CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC GAG AAG CAG AAA AAG AAG TIC TGG gga ATC AAG AAA GTA //GCA ACC GTA AAG GGC AAG ACC CAG ATG CTG GGT CTG

1020 1140 1200 1260 1080 900 ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG TTCAGCCCTA TATATATGCT GTATCTTTTA AGAGTATAAA AGGTTTGTGG TACTCACAAC TCCGATAGTA CGAAAAGAAA GAGACATGGA AAGGGAAGTT GGGCAAAATA CAAGCGTTAT CCTTGCCTTT AATAATGATT TTTGCCGTAT TGTTAAAGAA GTATCTCATA ACATCCCGAA AATCCACTTT TGAGGCAGTT TGCCGCTATA TGCTAGGGCA GCTGATAGGT AATTTTGGG CAGCTATGCG TTGTTCAAGT GGGACAAAGA TCAAGGGTAG CAGAGGAAAT AGCCAGAAAA TTGACCCGAT TATTGAGGAG ATAAAGGCAA TAAAGGGCGA TACCCTTTGC AGGGCGAGAT AAAATATCGA TTGATTTGCC CAATGGAAGA AGCTGGCAAA TCGTGGAGTG CTGATGAGGA ACGATGTTGC CCATACTCGG GGAGACGAGG AGCTTAAGCT CGTATACGCT CAATAATAGT GAATTTGGAA ATTCTTCCCC ATGGAAGCTG GACCCTCATT GTCAGGAAAA CAAGACXXXC GAATATGACA GGCCAGAGTA ATCACATGGA ATAAAGCGTT GGGGACAATT GCTGTGGAAA AACCAAAAGC AAATTAGGAG GCCCAGTACT ACCGGCAACC CCGAACAAAC CCTGGGAGGA TATGTAAAAG TGTAAGAATT SCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA GTCTTAGGAA AACCTCCCAA CTGTACCCTT TTTATTCCCT GAAAAACTA AATAGAACTT TGACATTTAC TGAGGGAGAT AAGAGAAATG AACTTACAAT AAGGACGATA GAGATCAAGC ATACCCTTGA AAAAGAGGGC CTTTCCGGGC TGCAGTGAAA CGAGCATCCC TCCCATGGAG TGATAGTTTT TGAACTTGCA TTTCCGCAGT AGTTCGGCTT GGGAGTTTAA ATGACTCCGC CAGCTGTGGT ATGAAGAAGA TGTCCAATGA ATGTGATAAT AAAAGCTGGG AGAGGATGGG CAGTTGTGCG TTTTAGGAAA AAGAAAGCAT TCGGGAAGGA GGGACGTCTC ACGCGAGGAA GAACAACTTA TTTATTTGGA TCTGCAAGGA GAGTGCTCGA AGCTCATTT AGGGCTTGAT CGTTTTATCA STATCCCCAG CTTCTCAAAG GTCGATGTTG AAACGGGCAG **TATGAAGCAG** TGGGAAACAG GGATATAGGT AAAGAGAACG AGGGAACATC GATATTGAAA AGTTATGCCG AAAGACCCCG CCCAAGATTC AGGGTGGCAT SAAAATATCA AAAACTGTGA GAAGTCTGGA CTCATAGACA GATCTTTCC ACGTATGAGC CAAAGTGTAT CGGCGCTTAA

FIGURE 17MMM (CONT.)

2100 1680 1740 1800 1860 1920 1980 2040 2160 GCTTGAGCTT TGCAGTCATA TTGGAGTGAG ACCGGGCACA TAAGGTTCTT AAGTGTTGAA GGTTCCACTT AGCCATTGGC CGGCTATATG CGCATGGGGG ACTCATTAAA AATTTTACTT AAACCAAGTT TTTAAGGTAT AGGACTACAA TAAAAGTGAA TTTGTTACAA AAAAGCGCTA TIGCTIGCAA ACAGCIAITA AACTCCAAAC TTCCAGGTCT TAAGGAGAGA TTAAAGAGGG CAAAATACAG GCGATAGGGT GAAAGGAGGA GAATGTGCTG AAAGCGTTAC ATAGAGGAAA AGTICGGCTI AAAAGCCTGA ACTACATAGA CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325 ATACCCGGGG GAGGCTATAC GAGAAAATAG AGGGATTTAA GCAAGAGGGA GATCCGGACT TTGGAAGTAG GGAAAGATAA TTTGGATACA AAACTACATA GCAGATTACC GATAAGAGAA GGCTATTAAA GTACTCGAAG TTATGCCACA GAGAGGATTC AACAAGGGGC AAAGGTTTTA AAGACTTGCC ACACAAGTAC ACTCGAAGCG AGATGTTGTA CAAAGGGAGC AGGAATTCCT CGATAGCAAA TACTTAGGAT GCAGGATAAC AGACTCAGGC AAGTTGTTAG ATCCTAGAAA ATAGGCAAAG TTATCCATGA AGGCAAGATG TAGAGATGAC CTGACGGCTT GCTTTTACTT ATATCGTTCT TTGCCGGCAG AAGAAAGCCA ATAGCTAAGG AAAGCTGTAG ACAGAATACG GGGTATCCTA AGACACTACA GATGAAGAGG CCTCATGTCG ATAATAAGCT ATGCTCGATT GAGTATGAGG GAAAAGCTTG TATGCGGACA

Figure 17NNN

Vent DNA POLYMERASE - Sso7d FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 71) CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG,

900 9 TATTGAGGAG ATAAAGGCCAA TAAAGGGCGA GAGACATGGA CAAGCGTTAT ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG TATATATGCT AAGGGAAGTT GGGCAAAATA CCTTGCCTTT AATAATGATT TTTGCCGTAT TGTTAAAGAA GTATCTCATA ACATCCCGAA AATCCACTTT TGAGGCAGTT TTCAGCCCTA AATTTTTGGG TACCCTTTGC AGGGCGAGAT TTGTTCAAGT GGGACAAAGA TCAAGGGTAG CGTATACGCT TCCCATGGAG GGAGACGAGG AGCTTAAGCT AAAATATCGA TTGATTTGCC CAGCTATGCG CAAGACXXXC GTCAGGAAAA CAGTIGIGG AAGGACGATA AACCICCCAA GAATATGACA GACCCTCATT GAATTTGGAA ATCACATGGA GTCTTAGGAA GCTGTGGAAA AAGAGAAATG ATAAAGCGTT GGGGACAATT AATAGAACTT TGACATTTAC AACTTACAAT TGAGGGAGAT TGCAGTGAAA CGAGCATCCC GGCCAGAGTA TGATAGTTTT AAAAGCTGGG AGTTCGGCTT ATGTGATAAT CAGCTGTGGT GGGAGTTTAA GAGTGCTCGA AGAGGATGGG ATGACTCCGC AGCTCATTT AGGCCTTGAT CGTTTTATCA TGTCCAATGA ATGAAGAAGA CTTCTCAAAG AGTTATGCCG GTCGATGTTG AAAGACCCCG AAACGGGCAG AAAGAGAACG AAAACTGTGA GAAGTCTGGA AGGGAACATC CTCATAGACA GATATTGAAA CCCAAGATTC GATCTTTCC

FIGURE 17NNN (CONT.)

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1800
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                                                                                                               TCCGATAGTA
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                                                                                                                                                                                                                                                                                                                AGCCATTGGC
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                                               GTATCTTTTA
                                                                                               TACTCACAAC
                                                                                                                                GGACTTAATT
                                                                                                                                                CGAAAAGAAA
                                                                                                                                                                CGGCTATATG
                                                                                                                                                                                                TAAGGTTCTT
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  TGCCGCTATA
                  CAATGGAAGA TGCTAGGGCA
                                 GCTGATAGGT
                                                                AGAGTATAAA
                                                                                AGGTTTGTGG
                                                                                                                                                                                                                  ACTCATTAAA
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                                                                                                                                                                                                                                                                                                                GCAGATTACC AGGGATTTAA AGGACTACAA
                                                                                                                                                                                                                                                                                                                                 AAGACTTGCC GCAAGAGGGA TAAAAGTGAA
TITIAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT
                                                               TGAACTTGCA CCGAACAAAC CTGATGAGGA
                                                                               AGCCAGAAAA
                                                                                                                                               TTGACCCGAT
                                                                                                                                                                GGCTATTAAA TTGCTTGCAA ACAGCTATTA
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                                 TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA
                                               TCGTGGAGTG
                                                                                                CAATAATAGT
                                                                                                               ACGATGTTGC
                                                                                                                                CCATACTCGG
                                                                                                                                                                                GTACTCGAAG GAATGTGCTG AAAGCGTTAC
                                                                                                                                                                                                GATAAGAGAA ATAGAGGAAA AGTTCGGCTT
                                                                                                                                                                                                                                                                                                                                                  GCGATAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                  CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //
                                                                               CCTGGGAGGA TATGTAAAAG
                                                                                                                                                                                                                 ATACCCGGGG
                                                                                                                                                                                                                                                                GCAGGATAAC AACAAGGGGC TTGGAAGTAG
                                                                                                                                                GAAGAAATG AAATCCACAA
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                                               ACCGGCAACC
                                                                                                               TGTAAGAATT
                                                                                                                                 TTTATTCCCT
                  AAGAAAGCAT GAAAAACTA GCCCAGTACT
                                                                                                 CTGTACCCTT
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                                                                                                                                                                                                                                                                                                 AGATGTTGTA
                                                                                                                                                                                                                                                                                 AAAGGTTTTA
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                                               GAGATCAAGC
                                                                                                               AAAAGAGGC
                                                                                                                                CTTTCCGGGC
                                                                                               TTTCCGCAGT
                                                                                                                                                                                                                                                                                                                                                                  ATCCTAGAAA
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                                                                                                                ATACCCTTGA
                                                                                                                                                                                 AGGCAAGATG
                                                                                                                                                                                                                                                 GCTTTTACTT
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                                                                                                TTTATTTGGA
                                                                                                                                                                                                                 CTGACGGCTT
                                                                                                                                                                                                                                                                                                                                                 ATATCGTTCT
                                                 GGGACGTCTC
                                                                ACGCGAGGAA
                                                                                                                                 TCTGCAAGGA
                                                                                                                                                                ATAGGCAAAG
                                                                                                                                                                                                TAGAGATGAC
                                                                                 GAACAACTTA
                                                                                                                                                AAGATATAAA
   TATGAAGCAG
               TGGGAAACAG
                                                               AGGGTGGCAT
                                                                                               GAAAATATCA
                                                                                                               GTATCCCCAG
                                                                                                                                                GCAATGAGGC
                                                                                                                                                                                 GGGTATCCTA
                                                                                                                                                                                                 AGACACTACA
                                                                                                                                                                                                                                AAGAAAGCCA
                                                                                                                                                                                                                                                                                 ATAGCTAAGG
                                                                                                                                                                                                                                                                                                                GAAAAGCTTG
                                                                                                                                                                                                                                                                                                                                 CCTCATGTCG
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                                                                                                                                                                                                                                                                                                                                                                  ACAGAATACG
                                                                                                                                                                                                                                                                                                                                                                                  TTGCCGGCAG
                                 ACGTATGAGC
                                                                                                                                GGATATAGGT
                                                                                                                                                                ATGCTCGATT
                                                                                                                                                                                                                  TATGCGGACA
                                                                                                                                                                                                                                                                                                AAAGCTGTAG
                                               CAAAGTGTAT
                                                                                 CGGCGCTTAA
                                                                                                                                                                                                                                                 GAGTATGAGG
                                                                                                                                                                                                                                                                 GATGAAGAGG
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CIG ACC TAC GAC GAG GAA AAG GAC GCG CCG AAG GAG GTA GAC ATC ATC TCC TTC GAA AAA GAG TAC AAA GGC GAA GTG GGC AAG ATG GGT GCG GTA AGC CAG AAA AAG CGT CGT AAG TTC AAG GAG ATC AAG AAA GTA TGG ACC GGC CIG // GCA ACC GTA AAG AAG CTG CAG ATG GGT GGC

Figure 17000

Deep Vent- Smod7 DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 71)

FIGURE 17000 (CONT.)

E CODONS FOR ARGININE)	rcaag 60	12	ATGGG 180			GGTAC 360	CATTT 420	IGATA 480		GGGAG 600		CAAAG 720	ACCTC 780							AGGGG 1200			-													AGGAG 2160		AGAAG 2280	2328
POSSIBLE GOTTO	GATTTTCAAG		A GAGGCATGGG	G GAGGCCGATT	G GGATAAGATA	C GAAGAGGTAC	T GCTCGCATTT	T TATAATGATA	A TCTCCCGTAC	T GATAAGGGAG	C CTATCTAGIT	G TGAGCCAAAG	A CTTTGACCTC	C AGTTTATGAG	A GGCCTGGGAG	A GGTAACGTAC	_	T CCTCAGGAAG	A CGAGAGAAGG	T CTGGGAGGGG	-		•	_	_	•	T CTTATACATA			_	G CGAAATAGCC	T TGAGGAGGCA	C TCCAGAAAAG	T AGGTCCGCAC	G CATGGTGATA	T TGCAGAGGAG		G GTGGCAGAAG	
CGT (ALL	CGATTATAAG	TTAGACCTTA	TAACCGCCGA	AGTTCCTGGG	CCGCAATAAG	TTCCGTTCGC	AGCTCAAGTT	AGGGGCCCAT	AAAAGATCGA	TCCTCAAGGT	TCGACCTTCC	GGGACGGTAG	GAAGGATACA	CCCTCGAGGC	AGATAGCTGA	AGGATGCAAA	CAAGGTTAGT	AGTGGTACCT	AGAGGGAGTA	AGAAAGGGCT	TAATCACCCA	TCGCCCCAGA	TCAAGAGGTT	CAATCGAGAA	ATTATGGGTA	TTACGGCCTG	GGTTCAAAGT	CCGAGGAGAT	GGCTGTTGGA	AGTATGCGTT	GGGACTGGAG	ATGGCAACGT	ACGAAATACC	ACAAGGCTAT	TGAGGCCTGG	GGGCTATCCT	TAGAAAATCA	AAGACCTCAG	AGAAG
CGC, CGG,	GATGGGAAGC	GACAGAAACT	GTTAGGAAGA	GTAAGGAAGA	CAGGACXXXC	GAGTACGACA	GGCGATGAAG	GAGTTCGCGA	ATAACGTGGA	ATAAAGCGGT	GGCGATTCTT	CCCCTGGGAA	GAGATAAAGG	CCAACATACA	TACGCTCACG	TATTCAATGG	GCCCAGCTTT	AACTTGGTGG	AAGCCGGATG	AAGGAGCCGG	CCCTCGATAA	GAATACGATG	CCCAGCCTGC	TCTAAAGACC	GCAAACAGCT	GCAGAGAGCG	GAAAAGTTCG	GGGCCAAAAC	AAGCTCCCAG	ACGAAGAAGA	ATAGTCAGGA	ATCCTAAAGC	CTGAGCAAGT	CTTCACGAGT	GGAGTAAAGG	ATAAGCAAGA	GAGTATTACA	TACAGGAAAG	AACATCAAGA
, AGG, CGA,	ATCAC	GGTTGAGTAC	GATTGATGAG	TGCCGAAAAG	TGAACACCCT	TGACATCTTT	TCCAATGGAA	CGAAGGGGAG	AGCCAAAGTC	GAGGGAGATG	TACCTACAAC	GATAAAGCTA	GACAGCGGTG	GATAAACCTC	GGAGAAAGTT	AGTTGCAAAG	CCCAATGGAG	TTCAACTGGC	GGCTCCAAAC	GGGATACGTT	GAGCCTGTAC	AGGGTGTAGG	GGGGTTTATC	GATGAAAGCT	CAAAATCCTG	TAAGGAGTGC	GGAACTGGAG	CACAATTCCT	TATAAACGCC	GITCLICGIG	GGGGCTTGAA	CCTAGAGGCT	AACTGAAAAG	CACGAGGCCC	AGCCGCTAGA	AGACGGGCCA	GTATGACGCT	GGCCTTTGGG	GGCATGGCTT
X	CGCTGACTA		ATGACTCGCA	GAATTATAGA	GGCTGTACTT	CCGCAGTTAT	AAGGCCTAAT	CCCTCTATCA	ATGAGGAAGA	TTTCCAGCGA	ATGTTATAAT	AAAAGCTCGG	TTGGGGATAT	TTAGGAGAAC	GAAAGCCAAA	GACTGGAGAG	GGGAGTTCTT	TTTCTAGGTC	GGAATGAATT	GCTACGCTGG	TAGATTTCAG	TGAACAGGGA	AGGACTTCCC	TAAAAAGGAA	AACGGGCAAT	GTTGGTACTG	TCGTAAGGAA	GACTCTACGC	TCGTAGATTA	ACGTGAGAGG	TAATCACTAG	AAGCAAAAGT	TTAAGGAGGT	ACGAGCAGAT	CAAAAAGGTT	TGCTGAGGGG	GGAAGCATAA	GAATATAGA	CAGGTCTTAC
V93R MUTANT:	PACTTG			AAGATAGTGA	GAGGTATGGA	AGAGAGCATT	CTAATAGACA	GACATAGAAA	AGCTATGCTG	GTCGAGGTAG	AAAGATCCCG	AAGAGGGCCG	ATGCAGAGGC	TACCACGTGA	GCAATCTTCG	ACTGGAAAGG	GAGCTCGGTA	CTGTGGGATG	GCCTACGAGA	CTAAGGGAGA	TTAGTTTCCC	CCGGATACGC	AAGTTCTGCA	AGGCAAGAAA	GATTACAGGC	GCAAAAGCCC	TATATAGAGT	GACACAGATG	GCCCTAGAGT	GAGGGCTTCT	GAAGGGAAGA	AAAGAAACCC	GTAAAGATAG	CTAGTTATTT	GTTGCCGTGG	GGGTACATAG	TTCGATCTCA	GCCGTTCTTA	ACTAAACAGA

FIGURE 17000 (CONT.)

CTG AAG ggG GAG TCC GAG GCG CCG AAG GTA GAC ATC TAC GAC ACC GAA AAA GAG GGC AAG ATG ATC TCC TTC GAA AAG GAC GGC GAA GCG GTA AGC ATG CTG GAG AAG CAG AAA AAG // TAC AAA GTG GGTAAG CGI CGI TGG GGC AAA GTA ACC GTA AAG AAG ATC AAG ggc CTG CAG // GCA ACC GGT

Figure 17PPP

Ssod7 - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 38) Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 37)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) GAG (ALL CODONS FOR GLUTAMIC ACID) V93E MUTANT: XXX = GAA,

CTG TIC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC AIC TCC AAG TGG CGI GIG GGC AAG AIG AIC ICC IIC ACC IAC GAC GAG GGC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG GAG AAG CAG AAA AAG TGG GTA AAG ATC AAG AAA GTA GGT GGC AAG ACC CTG CAG ATG CTG //GCA ACC

180 300 360 420 480 540 900 999 720 780 240 ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG GGATAAGATA GAAGGATACA CTTTGACCTC GAGGCATGGG GAGGCCGATT GAAGAGGTAC TCTCCCGTAC GATAAGGGAG GCTCGCATTT TATAATGATA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TTAGACCTTA TAACCGCCGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG CCGCAATAAG AGGGCCCAT GGGACGGTAG TICCGTICGC AGCTCAAGTT TCCTCAAGGT TCGACCTTCC GGTTGAGTAC GACAGAAACT GTTAGGAAGA GAGTACGACA GGCGATGAAG GAGTTCGCGA TTGGGGATAT GACAGCGGTG GAGATAAAGG CAGGACXXXC ATAAAGCGGT GGCGATTCTT CCCCTGGGAA GATTGATGAG TGAACACCCT CGAAGGGGAG GAGGGAGATG GATAAAGCTA TGACATCTTT TCCAATGGAA TACCTACAAC AAAAGCTCGG GAATTATAGA ATGAGGAAGA GCGAGTTTAA GGCTGTACTT CCGCAGTTAT AAGGCCTAAT ATGTTATAAT ATGACTCGCA TTTCCAGCGA CCCTCTATCA AAAGATCCCG ATGCAGAGGC CTCCTCAAAG CTAATAGACA AGCTATGCTG GTCGAGGTAG AAGAGGCCG AAAGAAAACG AAGATAGTGA AGAGAGCATT GACATAGAAA GAGGTATGGA

FIGURE 17PPP (CONT.)

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1320
                                                                                                                      1380
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                                                     1080
                                                                  1140
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                                                                                             1260
CCAACATACA CCCTCGAGGC AGTTTATGAG
             TACGCTCACG AGATAGCTGA GGCCTGGGAG
                                                     CCTCAGGAAG
                                                                                            TAACGTCTCA
                                                                                                                                   GAAGATGCTT
                                                                                                                                                              GGGGAGGGAA
                                                                                                                                                                           CTTATACATA
                                                                                                                                                                                         AAAGAAGAAA
                                                                                                                                                                                                       GCTTGAGTAC
                                                                                                                                                                                                                   GATAGATGAG
                                                                                                                                                                                                                                CGAAATAGCC
                                                                                                                                                                                                                                              TGAGGAGGCA
                                                                                                                                                                                                                                                           TCCAGAAAAG
                                                                                                                                                                                                                                                                        AGGTCCGCAC
                                                                                                                                                                                                                                                                                      CATGGTGATA
                                                                                                                                                                                                                                                                                                               GGTTTTACCT
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                           GGTAACGTAC
                                       CGGCCAGCCC
                                                                  CGAGAGAAGG
                                                                                 CTGGGAGGGG
                                                                                                         GGTTGGGCAC
                                                                                                                       ATTGGATGAA
                                                                                                                                                 TTATGGGTAC
                                                                                                                                                                                                                                                                        ACAAGGCTAT
                           TATTCAATGG AGGATGCAAA
                                                     AACTIGGIGG AGIGGIACCI
                                                                                             TAATCACCCA
                                                                                                                                                ATTATGGGTA
                                                                                                                                                              TTACGGCCTG
                                                                                                                                                                                        CCGAGGAGAT
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                                                                                                                                                                                                                                 GGGACTGGAG
                                                                                                                                                                                                                                                           ACGAAATACC
                                       CAAGGTTAGT
                                                                               AAGGAGCCGG AGAAAGGGCT
                                                                                                         TCGCCCCAGA
                                                                                                                      TCAAGAGGTT
                                                                                                                                   CAATCGAGAA
                                                                                                                                                                           GGTTCAAAGT
                                                                                                                                                                                                                                              ATGGCAACGT
                                                                                                                                                                                                                                                                                      TGAGGCCTGG
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                                                                    AGAGGGAGTA
                                                                                                                                                                                                       GGCTGTTGGA
                                                                                                                                                                                                                                                                                                   GGGCTATCCT
                                                                                                                                                                                                                                                                                                                 TAGAAAATCA
                                                                                                                                                                                                                                                                                                                                          ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA
                                                                  AAGCCGGATG
                                                                                            CCCTCGATAA
                                                                                                                                   TCTAAAGACC
                                                                                                                                                 GCAAACAGCT
                                                                                                                                                              GCAGAGAGCG
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                                                                                                                                                                                                                                              ATCCTAAAGC
                                                                                                                                                                                                                                                           CTGAGCAAGT
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                                                                                                         GAATACGATG
                                                                                                                      CCCAGCCTGC
                                                                                                                                                                                                                    ACGAAGAAGA
                                                                                                                                                                                                                                                                                      GGAGTAAAGG
                                                                                                                                                                                                                                                                                                  ATAAGCAAGA
                                                                                                                                                                                         GGGCCAAAAC
                                                                                                                                                                                                       AAGCTCCCAG
                                        GCCCAGCTTT
                                                                                                                                                                                                                                                                                                  AGACGGGCCA
                                        CCCAATGGAG
                                                     TTCAACTGGC
                                                                                                                                                                                                                    GTTCTTCGTG
                                                                                                                                                                                                                                                                                     CAAAAAGGTT AGCCGCTAGA
GATAAACCTC
             GGAGAAAGTT
                           AGTTGCAAAG
                                                                   GGCTCCAAAC
                                                                                GGGATACGTT
                                                                                                                                   GATGAAAGCT
                                                                                                                                                 CAAAATCCTG
                                                                                                                                                                                                       TATAAACGCC
                                                                                                                                                                                                                                              CCTAGAGGCT
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                                                                                                                                                                                         CACAATTCCT
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                                                                                              GAGCCTGTAC
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                                                                                                                                                 AACGGGCAAT
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                                                                                                                                                                             TCGTAAGGAA
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TTAGGAGAAC
                           GACTGGAGAG
                                                     TTTCTAGGTC
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                                         GGGAGTTCTT
                                                                   GGAATGAATT
                                                                                                                      AGGACTTCCC
                                                                                                                                    TAAAAAGGAA
             GAAAGCCAAA
                                                                                 GCTACGCTGG
                                                                                              TAGATTTCAG
                                                                                                                                                                                                                    GAGGCTTCT
                                                                                                                                                                                                                                GAAGGGAAGA
                                                                                                                                                                                                                                                                                                  GGGTACATAG
                                                                                                                                                                                                                                                                                                                TTCGATCTCA
                                                                                                                                                                                                                                                                                                                             GCCGTTCTTA
                                                                                                                                                 GATTACAGGC
                                                                                                                                                                                                                                                                         CTAGTTATTT
                                                     CTGTGGGATG
                                                                                                         CCGGATACGC
                                                                                                                                    AGGCAAGAAA
                                                                                                                                                               GCAAAAGCCC
                                                                                                                                                                             TATATAGAGT
                                                                                                                                                                                          GACACAGATG
                                                                                                                                                                                                      GCCCTAGAGT
                                                                                                                                                                                                                                              AAAGAAACCC
                                                                                                                                                                                                                                                            GTAAAGATAG
                                                                                                                                                                                                                                                                                       GTTGCCGTGG
 TACCACGTGA
              GCAATCTTCG
                                        GAGCTCGGTA
                                                                   GCCTACGAGA
                                                                                 CTAAGGGAGA
                                                                                            TTAGTTTCCC
                                                                                                                       AAGTTCTGCA
                           ACTGGAAAGG
```

Figure 17QQQ

JDF-3 - Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 71) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGAAAAAAATTCCTCGG ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCT CAGGTCTGTGGAGGTCTTGGGTCCTTTCACGCACCCGCAGGACXXXCCGGCAATCCGCGACAAATAAGGAAGCACCCCGCGGTCATCGACATCTACGAGTACGACATACCC

FIGURE 17000 (CONT.)

TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAAGAAGCTTAAACTCATGTCTTCGAGATQGAGACGCTCTACCACGAGGGGGAGAGAGTTTGGAA acgecegteectacetcaaggaecegagecegagetteteggacaatategtetatetagaettteetagtetetetageetateateateateaeceaeaegteeceagatae CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAATCTCCTCGATTACAGGCAACGGGGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT **ACTGGAGCGAGATAGCGAAGGAGGCGAGGCGAGGGTTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAATTGTCAGGGAAGTCACCGAAAAGCTGAGCAA** STTAAAATCCGGCCCGGAACTGTGATAAGCTACGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGGGGATTCCCTTCGACGACGACTTCGACCCGACGAGCACAAGTACGATG CGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTTGGCCGC **ACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTTCGGCAAGCCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCCGGCGAGGGGCTTTGAGAG GGTCGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCC** ATGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGGAGGTTGAGGAAAAGTTCGGTTTTAAAGTCCT GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCGCGGGCTTGAGATAGTCAGGCGCG GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAGCGTTTGGCCGACGC GCTTCTTGAGGGTCGTTAAGGAGGAGCCCGGACGTGCTGATAACATACAAACGGCGACGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGGAGCTTT **CCTCGGGAGGGACGGGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCCAGGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACCATAA** CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCCTTCTC GTGGCTGAAGCCGAAGGGGAAGAAGAAG/

TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC GGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG CAG ATG CTG GAG AAG CAG AAA AAG //GCA ACC GTA AAG ATC AAG AAA GTA GGT GGC AAG ACC CTG

Figure 17RRR

Sso7d - JDF-3 fusion protein

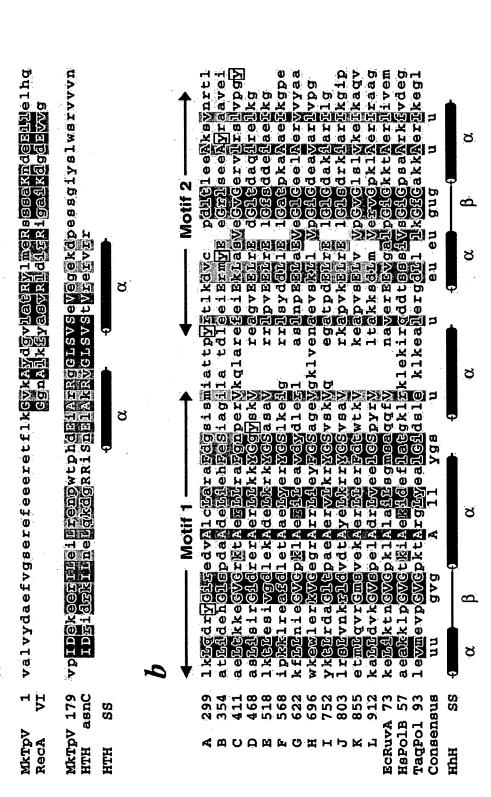
Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 40) Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 39)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC GGC CGT GCT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG GAG AAG CAG AAA AAG //GCA ACC GTA AAG ATC AAG AAA GTA CTG CAG ATG CTG GGC AAG ACC

acgecegtegetacetalageacegeagegegegegegegacaatategtegtetatetagactttegtagtetetad<mark>eet</mark>fteaateataateaceacaaegteegeagatae CAGGICTGIGGAGGICTGGGICCTCTACTTCACGCACCCGCAGGACXXXCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGGGTCATCGACATCTACGAGTACGACATACCC ttcgccaagcgctacctcatagacaagggcctaatcccgatggaaggtgaggaaggttaaactcatgtccttc<u>GaC</u>atc<u>GaG</u>acgctctaccacgaggagaagagtttggaa CCTCCCGACCTTACACCCTTGAGGCTGTATACGAGGCGGTTTTTCGGCAAGCCCCAAGGAGAGACTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAGAG GTCGCGCGCTACTCGATGGAGGGCGCGAGGGTTACCTACGAGGCAGGGAGTTCTTCCCCGATGGAGGCCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCC CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAATCTCCCTCGATTACAGGCAACGGGGGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGCTGAAAAACAGTCAAGAAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAAACTGCCGGCCTTCTC GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCGCGGGCTTGAGATAGTCAGGCGCG GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAAcGTTTGGCCGCCACAGAGGT CGGACTACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGC AGGGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGGTCGCGGGAGAAGGTGAAGAAAAAGTTCCTCGG GGCTTCTTGAGGGTCGTTAAGGAGGAGCCCGGACGTGCTGATAACATACAAACGGCGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGTAGC acctigggagggagggagcgaagatacagcgatgggggagacaggtttgcggtcgaggtgaagggcagggtacactttgacctttatccagtcataaaggcgcaccataa atgccagggcaagatggtactgcagggagtgcgccgagagcgttacggcatggggaagggaagtacatcgaaatggtcatcagagagcttgaggaaaagttcgsttttaaagtcct actggagcgagatagcgaagcgcaggcgagggttttggaggcgatactcaggcacgtgacgttgacgttgaagaggccgtcagaattgtcagggaagtcaccgaaaagctgagcaa a tga tocttga cgttga tta catca cogagaa tagaaa gococgtca toa goggtottcaagaa goacgagattca goattgaa tagaa cogogag t GTGGCTGAAGCCGAAGGGGGAAGAAGAAGTGA 75

73



79/80/81

81/17

83/84/85 86/87/88

89/90/91

92/93 94/95

102/103/104 105/106/107

99/100/101

86/16/96

11/112/113

108/109

(cited from Belova et al. (2001) Proc. Natl. Acad. Sci 98: 6015-6020) **EIGURE 18**

FIGURE 19

SEQ ID NO: 120 Synthetic Sso7d gene

GCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTAGACATCTCCAA GATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTACGACGAGGG CGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAGGACGCGCCGAAGGAGC TGCTGCAGATGCTGGAGAAG

SEQ ID NO: 121 The amino acid sequence of Sso7d.

ATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDAPKELLQ MLEKQKK

SEQ ID NO: 122 The DNA sequence encoding the Sso7d-ΔTaq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAG GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG TGTCACTAGTCCCAAGGCcCTGGAGGAGGCCCCCTGGCCCCGCCGGAAGGGGCC TTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCT GGCCGCCAGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCT CAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGC CCTGAGGGAAGGCCTTGGCCTCCGCCGGCGACGACCCCATGCTCCTCGCCTAC CTCCTGGACCCTTCCAACACCACCCCGAGGGGGTGGCCCGGCGCTACGGCGGG GAGTGGACGGAGGGGGGGGGGGGGCCGCCCTTTCCGAGAGGCTCTTCGCC AACCTGTGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAG GTGGAGAGCCCCTTTCCGCTGTCCTGGCCCACATGGAGGCCACGGGGGTGCGC CTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGCCGAGGAGATCGCCC GCCTCGAGGCCGAGGTCTTCCGCCTGGCCGCCACCCCTTCAACCTCAACTCCCG GGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAA GACGGAGAAGACCGCAAGCGCTCCACCAGCGCCGCCGTCCTGGAGGCCCTCCG CGAGGCCCACCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAGCT GAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCCAGGACGGCCG CCTCCACACCGCTTCAACCAGACGGCCACGGCCACGGCCAGGCTAAGTAGCTC CGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGC CGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAG ATAGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCT TCCAGGAGGGGGGACATCCACACGGAGACCGCCAGCTGGATGTTCGGCGTCC CCCGGGAGGCCGTGACCCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCG GGGTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGCTAGCCATCCCTTA CGAGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGG GCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGAC CCTCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGT GCGGGAGGCGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGC CGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGG GGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCAAAAGA GAGGGCGGAGGCCGTGGCCGGCTGGCCAAGGAGGTCATGGAGGGGGTGTATCC CCTGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGC CAAGGAGGCATTGATGGCCGCGGCGGAGGCGGCATCATCATCATCATTA A

SEQ ID NO: 123 The amino acid sequence of Sso7d-△Taq fusion protein

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDA PKELLQMLEKQKKGGGVTSPKALEEAPWPPPEGAFVGFVLSRKEPMWADLLALAA ARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLLDP SNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLWLYREVERPLS AVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERVLF DELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLIH PRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDYS QIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFGV LYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETLFGRR RYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLFPRLEEMGARMLL QVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKEGIDGR GGGGHHHHHH

SEQ ID NO: 124 The DNA sequence encoding the Sso7d-Taq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAG GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG TGTCACTAGTGGGATGCTGCCCCTCTTTGAGCCCAAGGGCCGGGTCCTCCTGGTG GACGGCCACCACCTGGCCTACCGCACCTTCCACGCCCTGAAGGGCCTCACCACCA GCCGGGGGAGCCGGTGCAGGCGGTCTACGGCTTCGCCAAGAGCCTCCTCAAGG CCCTCAAGGAGGACGGGGACGCGGTGATCGTGGTCTTTGACGCCAAGGCCCCCT CCTTCCGCCACGAGGCCTACGGGGGGTACAAGGCGGGCCGGGCCCCACGCCAG AGGACTTTCCCCGGCAACTCGCCCTCATCAAGGAGCTGGTGGACCTCCTGGGGCT GGCGCCTCGAGGTCCCGGGCTACGAGGCGGACGACGTCCTGGCCAGCCTGGC CAAGAAGGCGGAAAAGGAGGCTACGAGGTCCGCATCCTCACCGCCGACAAAG ACCTTTACCAGCTCCTTTCCGACCGCATCCACCTCCACCCCGAGGGGTACCT CATCACCCGGCCTGGCTTTGGGAAAAGTACGGCCTGAGGCCCGACCAGTGGGC CGACTACCGGGCCCTGACCGGGGACGAGTCCGACAACCTTCCCGGGGTCAAGGG CATCGGGGAGAAGACGCGAGGAAGCTTCTGGAGGAGTGGGGGAGCCTGGAAG CCCTCCTCAAGAACCTGGACCGGCTGAAGCCCGCCATCCGGGAGAAGATCCTGG CCCACATGGACGATCTGAAGCTCTCCTGGGACCTGGCCAAGGTGCGCACCGACCT GCCCTGGAGGTGGACTTCGCCAAAAGGCGGGAGCCCGACCGGGAGAGGCTTAG GGCCTTCTGGAGAGGCTTGAGTTTGGCAGCCTCCTCCACGAGTTCGGCCTTCTG GAAAGCCCCAAGGC:CTGGAGGAGGCCCCCTGGCCCCGCCGGAAGGGGCCTTC GTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCTGG CCGCCGCAGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCTCA GGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGCCC TGAGGGAAGGCCTTGGCCTCCGCCGGCGACGACCCCATGCTCCTCGCCTACCT CCTGGACCCTTCCAACACCACCCCGAGGGGGTGGCCCGGCGCTACGGCGGGGA GTGGACGGAGGGGGGGGGGGCGCCCTTTCCGAGAGGCTCTTCGCCAA CCTGTGGGGGAGGCTTGAGGGGGAGGGAGAGGCTCCTTTGGCTTTACCGGGAGGT GGAGAGGCCCCTTTCCGCTGTCCTGGCCCACATGGAGGCCACGGGGGTGCGCCT GGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGCCGAGGAGATCGCCCG CCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGG GACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAAG ACGGAGAAGACCGCAAGCGCTCCACCAGCGCCGCCGTCCTGGAGGCCCTCCGC GAGGCCCACCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAGCTG AAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCCAGGACGGCCGCC TCCACACCCGCTTCAACCAGACGGCCACGGCCACGGCCAGGCTAAGTAGCTCCG ATCCCAACCTCCAGA. ACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGCCG GGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAGAT AGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCTTC CAGGAGGGGGGGACATCCACACGGAGACCGCCAGCTGGATGTTCGGCGTCCCC CGGGAGGCCGTGGACCCCTGATGCGCCGGCGGCCAAGACCATCAACTTCGGG GTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGCTAGCCATCCCTTACG AGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGGGC

CTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGACCC
TCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGTGC
GGGAGGCGGCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGCCG
ACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGGGG
CCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCAAAAGAGA
GGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGGAGGGGTGTATCCCC
TGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGACTGGCTCTCCGCCA
AGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATCATCATCATTAA

SEO ID NO: 125 The amino acid sequence of Sso7d-Tag fusion protein.

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDA PKELLQMLEKQKKGGGVTSGMLPLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGE PVQAVYGFAKSLLKALKEDGDAVIVVFDAKAPSFRHEAYGGYKAGRAPTPEDFPRQ LALIKELVDLLGLARLEVPGYEADDVLASLAKKAEKEGYEVRILTADKDLYQLLSDR IHVLHPEGYLITPAWLWEKYGLR. PDQWADYRALTGDESDNLPGVKGIGEKTARKLL EEWGSLEALLKNLDRLKPAIREKILAHMDDLKLSWDLAKVRTDLPLEVDFAKRREP DRERLRAFLERLEFGSLLHEFGLLESPKALEEAPWPPPEGAFVGFVLSRKEPMWADL LALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLA YLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLWLYREV **ERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQL** ERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPL PDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQIRJRRAFIAEEGWLLVA LDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTI NFGVLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETL FGRRRYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLFPRLEEMGA RMLLQVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKE **GIDGRGGGGHHHHHH**

SEQ ID NO: 126 The DNA sequence encoding the Pfu-Sso7d fusion protein

ATGATTTTAGATGTGGATTACATAACTGAAGAAGGAAAACCTGTTATTAGGCTAT TCAAAAAGGGGAACGGAAAATTTAAGATAGAGCATGATAGAACTTTTAGACCAT ACATTTACGCTCTTCTCAGGGATGATTCAAAGATTGAAGAAGTTAAGAAAATAAC GGGGGAAAGGCATGGAAAGATTGTGAGAATTGTTGATGTAGAGAAGGTTGAGAA AAAGTTTCTCGGCAAGCCTATTACCGTGTGGAAACTTTATTTGGAACATCCCCAA GATGTTCCCACTATTAGAGAAAAGTTAGAGAACATCCAGCAGTTGTGGACATCT TCGAATACGATATTCCATTTGCAAAGAGATACCTCATCGACAAAGGCCTAATACC AATGGAGGGGAAGAAGAGCTAAAGATTCTTGCCTTCGATATAGAAACCCTCTA TCACGAAGGAGAAGAGTTTGGAAAAGGCCCAATTATAATGATTAGTTATGCAGA TGAAAATGAAGCAAAGGTGATTACTTGGAAAAACATAGATCTTCCATACGTTGA GGTTGTATCAAGCGAGAGAGAGATGATAAAGAGATTTCTCAGGATTATCAGGGA GAAGGATCCTGACATTATAGTTACTTATAATGGAGACTCATTCGACTTCCCATAT TTAGCGAAAAGGGCAGAAAAACTTGGGATTAAATTAACCATTGGAAGAGATGGA AGCGAGCCCAAGATGCAGAGAATAGGCGATATGACGGCTGTAGAAGTCAAGGG AAGAATACATTTCGACTTGTATCATGTAATAACAAGGACAATAAATCTCCCAACA TACACACTAGAGGCTGTATATGAAGCAATTTTTGGAAAGCCAAAGGAGAAGGTA TACGCCGACGAGATAGCAAAAGCCTGGGAAAGTGGAGAGAACCTTGAGAGAGTT GCCAAATACTCGATGGAAGATGCAAAGGCAACTTATGAACTCGGGAAAGAATTC CTTCCAATGGAAATTCAGCTTTCAAGATTAGTTGGACAACCTTTATGGGATGTTT AAAGAAACGAAGTAGCTCCAAACAAGCCAAGTGAAGAGGAGTATCAAAGAAGG CTCAGGGAGAGCTACACAGGTGGATTCGTTAAAGAGCCAGAAAAGGGGTTGTGG GAAAACATAGTATACCTAGATTTTAGAGCCCTATATCCCTCGATTATAATTACCC ACAATGTTTCTCCCGATACTCTAAATCTTGAGGGATGCAAGAACTATGATATCGC TCCTCAAGTAGGCCACAAGTTCTGCAAGGACATCCCTGGTTTTATACCAAGTCTC

TTGGGACATTTGTTAGAGGAAAGACAAAAGATTAAGACAAAAATGAAGGAAACT TTAGCAAATTCTTTCTACGGATATTATGGCTATGCAAAAGCAAGATGGTACTGTA AGGAGTGTGCTGAGAGCGTTACTGCCTGGGGAAGAAAGTACATCGAGTTAGTAT GGAAGGAGCTCGAAGAAAAGTTTGGATTTAAAGTCCTCTACATTGACACTGATG GTCTCTATGCAACTATCCCAGGAGGAGAAAGTGAGGAAATAAAGAAAAAGGCTC TAGAATTTGTAAAATACATAAATTCAAAGCTCCCTGGACTGCTAGAGCTTGAATA TGAAGGGTTTTATAAGAGGGGATTCTTCGTTACGAAGAAGAGGTATGCAGTAAT AGATGAAGAAGGAAAAGTCATTACTCGTGGTTTAGAGATAGTTAGGAGAGATTG GAGTGAAATTGCAAAAGAAACTCAAGCTAGAGTTTTGGAGACAATACTAAAACA CGGAGATGTTGAAGAAGCTGTGAGAATAGTAAAAGAAGTAATACAAAAGCTTGC CAATTATGAAATTCCACCAGAGAAGCTCGCAATATATGAGCAGATAACAAGACC ATTACATGAGTATAAGGCGATAGGTCCTCACGTAGCTGTTGCAAAGAAACTAGCT GCTAAAGGAGTTAAAATAAAGCCAGGAATGGTAATTGGATACATAGTACTTAGA GGCGATGGTCCAATTAGCAATAGGGCAATTCTAGCTGAGGAATACGATCCCAAA AAGCACAAGTATGACGCAGAATATTACATTGAGAACCAGGTTCTTCCAGCGGTA CTTAGGATATTGGAGGGATTTGGATACAGAAAGGAAGACCTCAGATACCAAAAG ACAAGACAAGTCGGCCTAACTTCCTGGCTTAACATTAAAAAATCCGGTACCGGC GGTGGCGGTGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTAGA CATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTAC GACGAGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAGGACGCGCC GAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGTGA

SEQ ID NO: 127 The amino acid sequence of the Pfu-Sso7d fusion protein

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERH GKIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFA KRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGPIIMISYADENEAKVITWKNID LPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGS EPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEI AKAWESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGN LVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESYTGGFVKEPEKGLWENIVYLDFR ALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIKTK MKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIE LVWKELEEKFGFKVLYIDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYE GFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDWSEIAKETQARVLETILKHGDVEE AVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVKIKPG MVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKED LRYQKTRQVGLTSWLNIKKSGTGGGGATVKFKYKGEEKEVDISKIKKVWRVGKMIS FTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKK

SEQ ID NO: 128 The DNA sequence encoding the Sac7d-\DaragetaTaq fusion protein

atgattacga attcgacggt gaaggtaaag ttcaagtata agggtgaaga gaaagaagta gacacttcaa agataaagaa ggtttggaga gtaggcaaaa tggtgtcctt tacctatgac gacaatggta agacaggtag aggagctgta agcgagaaag atgctccaaa agaattatta gacatgttag caagagcaga aagagagaag aaaggcggcg gtgtcactag ccccaaggcc ctggaggagg ccccctggcc cccgccggaa ggggccttcg tgggctttgt gctttcccgc aaggagccca tgtgggccga tcttctggcc ctggccgccg ccaggggggg ccgggtccac egggeeeeg ageettataa ageeeteagg gaeetgaagg aggegegggg gettetegee aaagacctga gegttetgge eetgagggaa ggeettggee teeegeeegg egaegaeeee atgetecteg cetacetect ggaccettee aacaccacce cegaggggt ggeceggege tacggcgggg agtggacgga ggaggcgggg gagcgggccg ccctttccga gaggctcttc gccaacctgt gggggaggct tgagggggag gagaggctcc tttggcttta ccgggaggtg gagaggeece ttteegetgt cetggeecac atggaggeea egggggtgeg cetggaegtg gcctatctca gggccttgtc cctggaggtg gccgaggaga tcgcccgcct cgaggccgag gtetteegee tggeeggeea eecetteaac etcaacteee gggaecaget ggaaagggte ctctttgacg agctagggct tcccgccatc ggcaagacgg agaagaccgg caagcgctcc accagegeeg cegteetgga ggeeeteege gaggeeeace ceategtgga gaagateetg cagtaccggg agctcaccaa gctgaagagc acctacattg accccttgcc ggacctcatc

SEQ ID NO: 129 The amino acid sequence of the Sac7d-ΔTaq fusion protein

MITNSTVKVKFKYKGEEKEVDTSKIKKVWRVGKMVSFTYDDNGKTGRGAVSEKDA PKELLDMLARAEREKKGGGVTSPKALEEAPWPPPEGAFVGFVLSRKEPMWADLLAL AAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLL DPSNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLWLYREVERP LSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERV LFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLI HPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDY SQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFG VLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETLFGR RRYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLFPRLEEMGARML LQVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKEGIDG RGGGGHHHHHH

SEQ ID NO: 130 The DNA sequence encoding the PL-ΔTaq fusion protein

ATGATTACGAATTCGAAGAAAAAGAAAAAGAAAAAGCGTAAGAAACGCAAAAA GAAAAAGAAAGCGGCGGTGTCACTAGTGGCGCAACCGTAAAGTTCAAGTACAA AGGCGAAGAAAAAGAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGG GCAAGATGATCTCCTTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTG CGGTAAGCGAAAAGGACGCCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAG AAAAAGGCCGCGGTGTCACCAGTCCCAAGGCCCTGGAGGAGGCCCCCTGGCCC CCGCCGGAAGGGCCTTCGTGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGG CCGATCTTCTGGCCCTGGCCGCCCAGGGGGGGCCCGGGTCCACCGGGCCCCCG AGCCTTATAAAGCCCTCAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAG CATGCTCCTCGCCTACCTCCTGGACCCTTCCAACACCACCCCGAGGGGGTGGCC CGGCGCTACGGCGGGGGTGGACGGAGGAGGCGGGGGGGCCGCCCTTTCC GAGAGGCTCTTCGCCAACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGCTCCTT TGGCTTTACCGGGAGGTGGAGAGGCCCCTTTCCGCTGTCCTGGCCCACATGGAGG CCACGGGGGTGCCCTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGC AACCTCAACTCCGGGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTC CCGCCATCGCCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCCGTCC TGGAGGCCCTCCGCGAGGCCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGG AGCTCACCAAGCTGAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCC CAGGACGGCCGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAG GCTAAGTAGCTCCGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGG CAGAGGATCCGCCGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTG GACTATAGCCAGATAGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAAC CTGATCCGGGTCTTCCAGGAGGGGGGGGACATCCACACGGAGACCGCCAGCTGG

FIGURE 19 (CONT.)

ATGTTCGGCGTCCCCGGGAGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAG
ACCATCAACTTCGGGTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGC
TAGCCATCCCTTACGAGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTT
CCCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGCAGGAGGCGGG
GGTACGTGGAGACCCTCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCC
GGGTGAAGAGCGTGCGGGAGGCGGCGAGCGCATGGCCTTCAACATGCCCGTCC
AGGGCACCGCCGCCGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCT
GGAGGAAATGGGGGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGA
GGCCCCAAAAGAGAGGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGG
AGGGGTGTATCCCCTGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGG
ACTGGCTCTCCGCCAAGGAGGGCATTGATGGCCGCGGCGGAGGCGGCATCATC
ATCATCATCATTAA

SEQ ID NO: 131 The amino acid sequence of PL- Δ Taq fusion protein

MITNSKKKKKKKKKKKKKKKKGGGVTSGATVKFKYKGEEKEVDISKIKKVWRVGK
MISFTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKKGGGVTSPKALEEAPWPPPEG
AFVGFVLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVL
ALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFAN
LWGRLEGEERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLE
AEVFRLAGHPFNLNSRDQLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIV
EKILQYRELTKLKSTYIDPLPDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTP
LGQRIRRAFIAEEGWLLVALDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMF
GVPREAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVR
AWIEKTLEEGRRRGYVETLFGRRRYVPDLEARVKSVREAAERMAFNMPVQGTAAD
LMKLAMVKLFPRLEEMGARMLLQVHDELVLEAPKERAEAVARLAKEVMEGVYPL
AVPLEVEVGIGEDWLSAKEGIDGRGGGGHHHHHHH

SEQ ID NO: 132 PRIMER L71F 5'-CCTGCTCTGCCGCTTCACGC-3'

SEQIDNO: 133 PRIMER L71R 5'-GCACAGCGGCTGGCTGAGGA-3'

SEQ ID NO: 134 PRIMER L18015F 15 5'-TGACGGAGGATAACGCCAGCAG-3'

SEQ ID NO: 135 PRIMER L23474R 5'-GAAAGACGA TGGGTCGCTAATACGC-3'

SEQ ID NO: 136 PRIMER L18015F 5'-TGACGGAGGATAAC GCCAGCAG-3'

SEQ ID NO: 137 PRIMER L29930R 5'-GGGGTTGGAGGTCAATGGGTTC-3'

SEQ ID NO: 138 PRIMER L3035OF 5'-CCTGCTCTGCCGCTTCACGC-3'

SEQ ID NO: 139 PRIMER L3512IR 30 5'- CACATGGTACAGCAAGCCTGGC-3'

SEQ ID NO: 140 PRIMER L2089F 5'-CCCGTATCTGCTGGGA TACTGGC-3'

SEQ IUD NO: 141 PRIMER L7112R 5'-CAGCGGTGCTGACTGAATCATGG-3'

SEQ ID NO: 142 PRIMER L3035OF 5 5'-CCTGCCTGCCGCTTCACGC-3'

SEQ ID NO: 143 PRIMER L40547R 5'-CCAATACCCGTTTCA TCGCGGC-3'

SEQ ID NO: 144 PRIMER H-Amelo-Y 5'-CCACCTCATCCTGG GCACC-3'

SEQ ID NO: 145 PRIMER H-Amelo-YR 5'-GCTTGAGGCCAACCATCAGAGC-3'

FIGURE 19 (CONT.)

SEQ ID NO: 146 Human beta-globin primer 536F 5'-GGTTGGCCAATCTACTCCCAGG-3'

SEQ ID NO: 147 Human beta-globin primer 536R 5'-GCTCACTCAGTGTGGCAAAG-3'

SEQ ID NO: 148 Human beta-globin primer 1408R 5'-GATTAGCAAAAGGGCCTAGCTTGG- 3'

Figure 20

PURIFIED THERMOSTABLE PYROCOCCUS FURIOSUS DNA POLYMERASE I

AMINO ACID SEQUENCE (SEQ ID NO: 62)

- Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile

 5 10 15
- Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
 20 25 30
- Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile 35 40 45
- Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
 50 60
- Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile 65 70 75 80
- Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile 85 90 95
- Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr 100 105 110
- Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125
- Met Glu Gly Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr 130 135 140
- Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile 145 150 155 160
- Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile 165 170 175
- Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190
- Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
 195 200 205
- Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu 210 215 220
- Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys 225 230 235 240
- Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile 245 250 255
- His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr 260 265 270

Tyr	Thr	Leu 275	Glu	Ala	Val	Tyr	Glu 280	Ala	Ile	Phe	Gly	Lys 285	Pro	Lys	Glu
Lys	Val 290	Tyr	Ala	Asp	Glu	Ile 295	Ala	Lys	Ala	Trp	Glu 300	Ser	Gly	Glu	Asn
Leu 305	Glu	Arg	Val	Ala	Lys 310	Tyr	Ser	Met	Glu	Asp 315	Ala	Lys	Ala	Thr	Tyr 320
Glu	Leu	Gly	Lys	Glu 325	Phe	Leu	Pro	Met	Glu 330	Ile	Gln	Leu	Ser	Arg 335	Leu
Val	Gly	Gln	Pro 340	Leu	Trp	Asp	Val	Ser 345	Arg	Ser	Ser	Thr	Gly 350	Asn	Leu
Val	Glu	Trp 355	Phe	Leu	Leu	Arg	Lys 360	Ala	Tyr	Glu	Arg	Asn 365	Glu	Val	Ala
Pro	Asn 370	Lys	Pro	Ser	Glu	Glu 375	Glu	Tyr	Gln	Arg	Arg 380	Leu	Arg	Glu	Ser
Tyr 385	Thr	Gly	Gly	Phe	Val 390	Lys	Glu	Pro	Glu	Lys 395	Gly	Leu	Trp	Glu	Asn 400
Ile	Val	Tyr	Leu	Asp 405	Phe	Arg	Ala	Leu	Tyr 410	Pro	Ser	Ile	Ile	Ile 415	Thr
His	Asn	Val	Ser 420	Pro	Asp	Thr	Leu	Asn 425	Leu	Glu	Gly	Сув	Lys 430	Asn	Tyr
Asp	Ile	Ala 435	Pro	Gln	Val	Gly	His 440	Lys	Phe	Cys	Lys	Asp 445	Ile	Pro	Gly
Phe	Ile 450	Pro	Ser	Leu	Leu	Gly 455	His	Leu	Leu	Glu	Glu 460	Arg	Gln	Lys	Ile
Lys 465	Thr	Lys	Met	Lys	Glu 470	Thr	Gln	Asp	Pro	Ile 475	Glu	ГÀЗ	Ile	Leu	Leu 480
Asp	Tyr	Arg	Gln	Lys 485	Ala	Ile	Lys	Leu	Leu 490	Ala	Asn	Ser	Phe	Tyr 495	Gly
Tyr	Tyr	Gly	Tyr 500	Ala	Lys	Ala	Arg	Trp 505	Tyr	Cys	Lys	Glu	Сув 510	Ala	Glu
Ser	Val	Thr 515	Ala	Trp	Gly	Arg	Lys 520	Tyr	Ile	Glu	Leu	Val 525	Trp	Lys	Glu
Leu	Glu 530	Glu	Lys	Phe	Gly	Phe 535	Lys	Val	Leu	Tyr	Ile 540	Asp	Thr	Asp	Gly
Leu 545	Tyr	Ala	Thr	Ile	Pro 550	Gly	Gly	Glu	Ser	Glu 555	Glu	Ile	Lys	Lys	Lys 560
Ala	Leu	Glu	Phe	Val 565	Lys	Tyr	Ile	Asn	Ser 570	Lys	Leu	Pro	Gly	Leu 575	Leu

Glu	Leu	Glu	Tyr 580	Glu	Gly	Phe	Tyr	Lys 585	Arg	Gly	Phe	Phe	Val 590	Thr	Lys	
Lys	Arg	Tyr 595	Ala	Val	Ile	Asp	Glu 600	Glu	Gly	Lys	Val	Ile 605	Thr	Arg	Gly	
Leu	Glu 610	Ile	Val	Arg	Arg	Asp 615	Trp	Ser	Glu	Ile	Ala 620	Lys	Glu	Thr	Gln	
Ala 625	Arg	Val	Leu	Glu	Thr 630	Ile	Leu	Lys	His	Gly 635	Asp	Val	Glu	Glu	Ala 640	
Val	Arg	Ile	Val	Lys 645	Glu	Val	Ile	Gln	Lys 650	Leu	Ala	Asn	Tyr	Glu 655	Ile	
Pro	Pro	Glu	Lys 660	Leu	Ala	Ile	Tyr	Glu 665	Gln	Ile	Thr	Arg	Pro 670	Leu	His	
Glu	Tyr	Lys 675	Ala	Ile	Gly	Pro	His 680	Val	Ala	Val	Ala	Lys 685	Lys	Leu	Ala	
Ala	Lys 690	Gly	Val	Lys	Ile	Lys 695	Pro	Gly	Met	Val	Ile 700	Gly	Tyr	Ile	Val	
Leu 705	Arg	Gly	Asp	Gly	Pro 710	Ile	Ser	Asn	Arg	Ala 715	Ile	Leu	Ala	Glu	Glu 720	
Tyr	Asp	Pro	Lys	Lys 725	His	Lys	Tyr	Asp	Ala 730	Glu	Tyr	Tyr	Ile	Glu 735	Asn	
Gln	Val	Leu	Pro 740	Ala	Val	Leu	Arg	Ile 745	Leu	Glu	Gly	Phe	Gly 750	Tyr	Arg	
Lys	Glu	Asp 755	Leu	Arg	Tyr	Gln	Lys 760	Thr	Arg	Gln	Val	Gly 765	Leu	Thr	Ser	
Trp	Leu 770	Asn	Ile	Lys	Lys	Ser 775										
PUR	IFIE	D TH	ERMO	STAB	LE P	YROC	CCU	s FUI	RIOS	JS DI	NA P	OLYM	ERAS:	ΕI		
NUC	LEOT:	IDE :	SEQU	ENCE	(SE	Q ID	NO:	61)								
ccc	tggt	cct q	gggt	ccac	at a	tatg	ttct	t act	tege	cttt	atg	aaga	atc (cccc	agtcgc	60
tct	aacci	tgg (gtta	tagt	ga ca	aaat	cttc	c tc	cacca	accg	ccc	aagaa	agg	ttatt	tctat	120
caa	ctcta	aca (cctc	ccct	at t	ttct	ctct	t at	gagai	ttt	taa	gtata	agt	tatag	gagaag	180
gtt	ttata	act (ccaa	actg	ag t	tagta	agat	a tgi	tggg	gagc	ata	atga	ttt	tagat	gtgga	240
tta	cata	act 9	gaag	aagg	aa a	acct	gtta	t tag	ggcta	attc	aaa	aaag	aga a	acgga	aaatt	300
taa	gata	gag (catg	atag	aa c	tttta	agac	c ata	acati	tac	gct	cttc	tca 🤉	gggat	gattc	360
aaa	gatt	gaa 🤄	gaag	ttaa	ga aa	aataa	acgg	g gga	aaag	gcat	ggaa	aaga	ttg '	tgaga	aattgt	420

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aataccaatg	gaggggaag	aagagctaaa	gattcttgcc	ttcgatatag	aaaccctcta	660
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agttacttat	aatggagact	cattcgactt	cccatattta	gcgaaaaggg	cagaaaaact	900
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tatgacggct	gtagaagtca	agggaagaat	acatttcgac	ttgtatcatg	taataacaag	1020
gacaataaat	ctcccaacat	acacactaga	ggctgtatat	gaagcaattt	ttggaaagcc	1080
aaaggagaag	gtatacgccg	acgagatagc	aaaagcctgg	gaaagtggag	agaaccttga	1140
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ccttccaatg	gaaattcagc	tttcaagatt	agttggacaa	cctttatggg	atgtttcaag	1260
gtcaagcaca	gggaaccttg	tagagtggtt	cttacttagg	aaagcctacg	aaagaaacga	1320
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tcgtggttta	gagatagtta	ggagagattg	gagtgaaatt	gcaaaagaaa	ctcaagctag	2100
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agtaatacaa	aagcttgcca	attatgaaat	tccaccagag	aagctcgcaa	tatatgagca	2220
gataacaaga	ccattacatg	agtataaggc	gataggtcct	cacgtagctg	ttgcaaagaa	2280
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tctaaccttt	ttctatgaaa	gaagaactga	gcaggaatta	ccagttcttc	cgttatttta	2640
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acaattttt	ccttgtatct	cctaatgtat	aagcaagcca	aaggagagta	gatgctacct	3060
ttccgggagt	tttgtattgc	tctagccaag	gtttgggatt	tttgaatcct	ttaactctgg	3120
aaagtataat	ttcaagctcc	ttcttcttca	tgacagatga	aaaattgttt	tgtctctttt	3180
taacttttác	agaaataact	gtctcaaatt	atgacaactc	ttgacatttt	tacttcatta	3240
ccagggtaat	gtttttaagt	atgaaatttt	tctttcatag	aggaggnnnn	nngtcctctc	3300
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gacactcaaa	taccagacga	caatggtgtg	ctcactcaag	ccccatatgg	gttgagaaaa	3420
gtagaagcgg	cactactcag	atgcttcccc	aggaatgagg	ttgttgtagc	tcntcccnga	3480
aagattgaga	tgttcttgg					3499